



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 115241

TO: Karen A Lacourciere

Location: rem/2d15/2c18

Art Unit: 1635

Monday, March 08, 2004

Case Serial Number: 09/848868

From: Alex Waclawiw

Location: Biotech-Chem Library

Rem 1A71

Phone: 308-4491

Alexandra.waclawiw@uspto.gov

Search Notes

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 22:57:56 ; Search time 343 Seconds
(without alignments)
222.938 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 cccggaagcagctctgc 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2001bs:*

6: Geneseq2002s:*

7: Geneseq2003as:*

8: Geneseq2003bs:*

9: Geneseq2003cs:*

10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	18	100.0	18	AA519106	AA519106 Human p53
2	18	100.0	36	AA519107	AA519107 Human p53
3	18	100.0	37	AA526511	AA526511 WO 990919
4	18	100.0	140	AAV17739	AAV17739 Human bre
5	18	100.0	255	AAQ74245	AAQ74245 p53 antic
6	18	100.0	255	AAV17740	AAV17740 Human bre
7	18	100.0	800	AA159673	AA159673 Human p53
8	18	100.0	1024	AB283767	AB283767 Toxicolog
9	18	100.0	1070	AA252304	AA252304 Human p35
10	18	100.0	1303	AA504533	AA504533 Human encod
11	18	100.0	1303	AB573327	AB573327 DNA encod
12	18	100.0	1303	AA549400	AA549400 Human p53
13	18	100.0	1307	AAAD00088	AAAD00088 Human tum
14	18	100.0	1307	ABX15394	ABX15394 Human p53
15	18	100.0	1317	AA132831	AA132831 Human p53
16	18	100.0	1317	AAV18151	AAV18151 Nucleotid
17	18	100.0	1317	AAV21414	AAV21414 Human p53
18	18	100.0	1317	AAV44695	AAV44695 Human wil
19	18	100.0	1317	AA584597	AA584597 Human p53
20	18	100.0	1317	AAAD1279	AAAD1279 Human p53
21	18	100.0	1317	AAAD43529	AAAD43529 Human p53
22	18	100.0	1760	AA179880	AA179880 DNA encod
23	18	100.0	1760	AA575765	AA575765 Human p53
24	18	100.0	1760	AA54029	AA54029 Human col
25	18	100.0	1760	ABAD0952	ABAD0952 Human p53
26	18	100.0	2451	AAAD22450	AAAD22450 HLA-B*46 T
27	18	100.0	2600	AA565699	AA565699 DNA encod
28	18	100.0	2600	AA567409	AA567409 DNA encod
29	18	100.0	2600	ABX09379	ABX09379 Human p53
30	18	100.0	2600	ABX09379	ABX09379 Human p53
31	18	100.0	2600	ABX09379	ABX09379 Human p53
32	18	100.0	2600	ABX09379	ABX09379 Human p53
33	18	100.0	2600	ABX09379	ABX09379 Human p53
34	18	100.0	2600	ABX09379	ABX09379 Human p53
35	18	100.0	2600	ABX09379	ABX09379 Human p53
36	18	100.0	2600	ABX09379	ABX09379 Human p53
37	18	100.0	2600	ABX09379	ABX09379 Human p53
38	18	100.0	2600	ABX09379	ABX09379 Human p53
39	18	100.0	2600	ABX09379	ABX09379 Human p53
40	18	100.0	2600	ABX09379	ABX09379 Human p53
41	18	100.0	2600	ABX09379	ABX09379 Human p53
42	18	100.0	2600	ABX09379	ABX09379 Human p53
43	18	100.0	2600	ABX09379	ABX09379 Human p53
44	18	100.0	2600	ABX09379	ABX09379 Human p53
45	18	100.0	2600	ABX09379	ABX09379 Human p53
46	18	100.0	2600	ABX09379	ABX09379 Human p53
47	18	100.0	2600	ABX09379	ABX09379 Human p53
48	18	100.0	2600	ABX09379	ABX09379 Human p53
49	18	100.0	2600	ABX09379	ABX09379 Human p53
50	18	100.0	2600	ABX09379	ABX09379 Human p53
51	18	100.0	2600	ABX09379	ABX09379 Human p53
52	18	100.0	2600	ABX09379	ABX09379 Human p53
53	18	100.0	2600	ABX09379	ABX09379 Human p53
54	18	100.0	2600	ABX09379	ABX09379 Human p53
55	18	100.0	2600	ABX09379	ABX09379 Human p53
56	18	100.0	2600	ABX09379	ABX09379 Human p53
57	18	100.0	2600	ABX09379	ABX09379 Human p53
58	18	100.0	2600	ABX09379	ABX09379 Human p53
59	18	100.0	2600	ABX09379	ABX09379 Human p53
60	18	100.0	2600	ABX09379	ABX09379 Human p53
61	18	100.0	2600	ABX09379	ABX09379 Human p53
62	18	100.0	2600	ABX09379	ABX09379 Human p53
63	18	100.0	2600	ABX09379	ABX09379 Human p53
64	18	100.0	2600	ABX09379	ABX09379 Human p53
65	18	100.0	2600	ABX09379	ABX09379 Human p53
66	18	100.0	2600	ABX09379	ABX09379 Human p53
67	18	100.0	2600	ABX09379	ABX09379 Human p53
68	18	100.0	2600	ABX09379	ABX09379 Human p53
69	18	100.0	2600	ABX09379	ABX09379 Human p53
70	18	100.0	2600	ABX09379	ABX09379 Human p53
71	18	100.0	2600	ABX09379	ABX09379 Human p53
72	18	100.0	2600	ABX09379	ABX09379 Human p53
73	18	100.0	2600	ABX09379	ABX09379 Human p53
74	18	100.0	2600	ABX09379	ABX09379 Human p53
75	18	100.0	2600	ABX09379	ABX09379 Human p53
76	18	100.0	2600	ABX09379	ABX09379 Human p53
77	18	100.0	2600	ABX09379	ABX09379 Human p53
78	18	100.0	2600	ABX09379	ABX09379 Human p53
79	18	100.0	2600	ABX09379	ABX09379 Human p53
80	18	100.0	2600	ABX09379	ABX09379 Human p53
81	18	100.0	2600	ABX09379	ABX09379 Human p53
82	18	100.0	2600	ABX09379	ABX09379 Human p53
83	18	100.0	2600	ABX09379	ABX09379 Human p53
84	18	100.0	2600	ABX09379	ABX09379 Human p53
85	18	100.0	2600	ABX09379	ABX09379 Human p53
86	18	100.0	2600	ABX09379	ABX09379 Human p53
87	18	100.0	2600	ABX09379	ABX09379 Human p53
88	18	100.0	2600	ABX09379	ABX09379 Human p53
89	18	100.0	2600	ABX09379	ABX09379 Human p53
90	18	100.0	2600	ABX09379	ABX09379 Human p53
91	18	100.0	2600	ABX09379	ABX09379 Human p53
92	18	100.0	2600	ABX09379	ABX09379 Human p53
93	18	100.0	2600	ABX09379	ABX09379 Human p53
94	18	100.0	2600	ABX09379	ABX09379 Human p53
95	18	100.0	2600	ABX09379	ABX09379 Human p53
96	18	100.0	2600	ABX09379	ABX09379 Human p53

CC is preferably a phosphorodiamidate-linked morpholino oligonucleotide.
 CC Such targeting is effective to inhibit natural mRNA splice processing,
 CC produce splice variant mRNAs, and inhibit normal expression of the
 CC protein. The present sequence is an antisense sequence described in the
 CC exemplification of the invention

XX Sequence 18 BP; 3 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
 DB 1 CCCGAGAGCAGTCTGGC 18

RESULT 2

AA519107 standard; DNA; 36 BP.

XX AA519107;

DT 15-MAR-2002 (first entry)

DE Human p53 coding sequence antisense sequence SEQ ID NO: 36.

XX Antisense; splice region; mRNA splice processing inhibition;

KM splice variant; protein expression inhibition; human; HIV-1; rat; ss.

XX Homo sapiens.

OS WO200183740-A2.

XX 08-NOV-2001.

PF 04-MAY-2001; 2001WO-US014410.

XX 04-MAY-2000; 2000US-0202376P.

PA (AVIB-) AVI BIOPHARMA INC.

PI Iversen PL, Hudziak R;

XX WPI; 2002-066533/09.

PT Splice-region antisense composition and method.

XX Claim 37; Page 23; 53pp; English.

CC The present invention relates to antisense compositions targeted to an
 CC mRNA sequence for a selected protein, at a region having its 5' end from
 CC 1 to about 25 base pairs downstream of a normal splice acceptor junction
 CC in the preprocessed mRNA. The antisense compound is RNase-inactive, and
 CC is preferably a phosphorodiamidate-linked morpholino oligonucleotide.
 CC Such targeting is effective to inhibit natural mRNA splice processing,
 CC produce splice variant mRNAs, and inhibit normal expression of the
 CC protein. The present sequence is an antisense sequence described in the
 CC exemplification of the invention

XX Sequence 36 BP; 6 A; 11 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 36;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
 DB 17 CCCGAGAGCAGTCTGGC 34

RESULT 3

AA26511/c

ID AAX26511 standard; DNA; 37 BP.

XX AAX26511;

XX 28-MAY-1999 (first entry)

DT WO 9909191 SeqID #13.

DE Cancer; treatment; vector; recombinase gene; transcription factor;
 KW selective cell killing; gene therapy; primer; ss.

XX Synthetic.

OS WO9909191-A1.

XX 25-FEB-1999.

PF 02-JUL-1998; 98WO-JP002993.

XX 20-AUG-1997; 97JP-00223651.

PA (DNAV-) DNAVEC RES INC.

PI Yokoi H, Takeda K, Hasegawa M;

XX WPI; 1999-181048/15.

PT Gene expression specific to cells free from specific transcription factor
 with constructed recombinase expression unit after infecting cells -
 PT allowing expression of target gene in gene therapy, particularly in
 cancer treatment.

XX Example 1; Page 16; 49pp; Japanese.

CC This invention describes a vector containing a recombinase gene which is
 CC controlled by (1) a promoter and action of which is in turn dependent on
 CC a specific transcription factor and (2) a desired gene to be expressed
 CC and two target sequences of the recombinase. Also described in the
 CC invention are (1) a host cell for introduction of the vector and (1) an
 CC in vitro technique in which killing of cells without the specific
 CC transcription factor is selectively performed after the vector is
 CC introduced into a host cell by an in vitro technique. The technique is
 CC used for gene therapy e.g. in cancer treatment. The products of the
 CC invention allow the use of a specific vector specifically and safely,
 CC there is little toxicity

XX Sequence 37 BP; 7 A; 13 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 37;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
 DB 30 CCCGAGAGCAGTCTGGC 13

RESULT 4

AAV17739 standard; cDNA; 140 BP.

XX AAV17739;

XX 14-AUG-1998 (first entry)

DE Human breast cancer related gene BC532L.

XX L-oncogene; diagnosis; treatment; ovarian cancer; antibody; antisense;

XX Homo sapiens.

XX Key Location/Qualifiers


```

FT CDS 4..138
FT /*tag= A
FT /product= "BC532L"
XX
XX PN WO9807851-A2.
XX
XX PD 26-FEB-1998.
XX
XX PF 22-AUG-1997; 97WO-EP004600.
XX
XX PR 22-AUG-1996; 96CA-02183900.
XX
XX PA (BERG/) BERGMANN J E.
XX PA (PRED/) PREDDIE E R.
XX
XX PI Bergmann JE, Preddie ER;
XX
XX WP1: 1998-169156/15.
XX
XX DR P-PSDB; AAW48346.
XX
XX PT Human breast cancer related genes - used for diagnosis, pre-symptomatic
XX detection and therapy of breast and ovarian cancers.
XX
XX PS Claim 2; Fig 1c; 96pp; English.
XX
XX CC Human breast cancer related genes, l-oncogenes (AAV17738-V17753), and the
XX proteins encoded can be used in the diagnosis and treatment of breast and
XX ovarian cancer. Antibodies and multiple antigenic peptide epitopes can be
XX used to detect the presence of the proteins. The antibodies can also be
XX used to block the activity of the proteins. Antisense molecules can be
XX used to prevent expression of the proteins
XX
XX SQ Sequence 140 BP; 29 A; 48 C; 42 G; 21 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCGAGAGCAGCTGCGC 18
DB 14 CCCGAGAGCAGCTGCGC 31

RESULT 5
AAQ74245
ID AAQ74245 standard; cDNA; 255 BP.
XX
XX AC AAQ74245;
XX
XX DT 25-MAR-2003 (revised)
XX DT 02-JUN-1995 (first entry)
XX
XX DE p53 antisense strand cDNA encoding protein BC538.1.
XX
XX KM BC534; BC538; BC538.1; p53 antisense strand; breast cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9421791-A1.
XX
XX PD 29-SEP-1994.
XX
XX PF 04-MAR-1994; 94WO-EP000651.
XX
XX PR 16-MAR-1993; 93US-00032843.
XX
XX PA (BERG/) BERGMANN J E.
XX PA (PRED/) PREDDIE E R.
XX
XX PI Bergmann JE, Preddie ER;
XX
XX WP1: 1994-357732/44.
XX
XX DR P-PSDB; AARS1627.

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XX
XX PR New p53 anti sense proteins - used to develop prods. for the diagnosis,
XX prediction and treatment of breast cancer and related cancers.
XX
XX PS Claim 1; Fig 1E; 46pp; English.
XX
XX CC AAQ74243, AAQ74244 and AAQ74245 are cDNA fragments of the p53 gene
XX antisense strand which encode AARS1625 (BC534), AARS1626 (BC538) and
XX AARS1627 (BC538.1) respectively. These proteins can be used to develop
XX products which can be used in the diagnosis and prediction of breast
XX cancer and other cancers associated with mutations of the p53 gene.
XX These cancers can be treated by providing the patient with an inhibitor
XX of the BC534, BC538 and BC538.1 genes, and the regulatory sequence
XX AAQ74246 (BC53/Reg). (Updated on 25-MAR-2003 to correct PM field.)
XX
XX SQ Sequence 255 BP; 58 A; 82 C; 66 G; 49 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCGAGAGCAGCTGCGC 18
DB 14 CCCGAGAGCAGCTGCGC 31

RESULT 6
AAV17740
ID AAV17740 standard; cDNA; 255 BP.
XX
XX AC AAV17740;
XX
XX DT 14-AUG-1998 (first entry)
XX
XX DE Human breast cancer related gene BC533L.
XX
XX KM l-oncogene; diagnosis; treatment; ovarian cancer; antibody; antisense;
XX ss.
XX
XX OS Homo sapiens.
XX
XX PH Key Location/Qualifiers
XX FT CDS 3..255
XX FT /*tag= A
XX FT /product= "BC533L"
XX
XX PN WO9807851-A2.
XX
XX PD 26-FEB-1998.
XX
XX PF 22-AUG-1997; 97WO-EP004600.
XX
XX PR 22-AUG-1996; 96CA-02183900.
XX
XX PA (BERG/) BERGMANN J E.
XX PA (PRED/) PREDDIE E R.
XX
XX PI Bergmann JE, Preddie ER;
XX
XX WP1: 1998-169156/15.
XX
XX DR P-PSDB; AAW48347.
XX
XX PT Human breast cancer related genes - used for diagnosis, pre-symptomatic
XX detection and therapy of breast and ovarian cancers.
XX
XX PS Claim 1; Fig 1e; 96pp; English.
XX
XX CC Human breast cancer related genes, l-oncogenes (AAV17738-V17753), and the
XX proteins encoded can be used in the diagnosis and treatment of breast and
XX ovarian cancer. Antibodies and multiple antigenic peptide epitopes can be
XX used to detect the presence of the proteins. The antibodies can also be
XX used to block the activity of the proteins. Antisense molecules can be
XX used to prevent expression of the proteins

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XX Sequence 255 BP; 58 A; 83 C; 65 G; 49 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 18; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAAAGCAGTCTGGC 18
 DB 14 CCGGAAAGCAGTCTGGC 31

RESULT 7
 AAT59673/c
 ID AAT59673 standard; DNA; 800 BP.
 AC AAT59673;
 AT 07-OCT-1997 (first entry)
 DE Human p53 gene fragment.
 XX
 XX Target nucleotide sequence; point mutation; analysis;
 KM Criminal investigation; parental determination; ss.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT exon 421..699
 FT /tag= a
 FT /number= 1
 FT /note= "Exon in which possible mutation sites occur"
 FT misc_difference 467
 FT /tag= b
 FT /note= "Wild-type A could be point mutated to T"
 FT misc_difference 605
 FT /tag= C
 FT /note= "Wild-type C could be point mutated to A"

MO9641001-A1.
 PD 19-DEC-1996.
 PF 05-JUN-1996; 96WO-US008759.
 PR 07-JUN-1995; 95US-00472239.
 PA (ONCO-) ONCOR INC.
 XX George AL, Bhattachar SK, Nazarenko I;
 DR WPI; 1997-099941/09.
 XX
 PT Analysis of target nucleotide sequence which exists in a first state or
 PT different second state - useful for determination of point mutation(s).
 XX
 PS Disclosure: Page 45-46; 78pp; English.

CC A novel method has been produced for analyzing a target nucleotide
 CC sequence. The target sequence having a first segment, a second segment
 CC and a third segment between the first and second, which is formed of at
 CC least one, but less than four different, nucleotide(s) where the third
 CC segment has a nucleotide or nucleotide sequence in a first state or
 CC different second state. The present sequence is a partial human p53 gene
 CC sequence which is used as an example of a target nucleotide sequence. The
 CC method can be used to analyse the entire sequence (portion) of a known
 CC gene and to analyse infectious disease or to determine if a sample is
 CC from a particular source, such as for criminal investigations or parental
 CC determination. Especially the method is used to determine the existence
 CC or absence of mutations consisting of one or a few nucleotides

Sequence 800 BP; 148 A; 252 C; 214 G; 186 T; 0 U; 0 Other;

QY 1 CCGGAAAGCAGTCTGGC 18
 DB 108 CCGGAAAGCAGTCTGGC 91

RESULT 8
 AB283767/c
 ID AB283767 standard; cDNA; 1024 BP.
 AC AB283767;
 AT 14-MAY-2003 (first entry)
 DE Toxicologically relevant human nucleotide sequence #926.
 XX
 XX Toxicologically relevant gene; toxicological response; gene; ss.
 KM
 XX
 OS Homo sapiens.
 PN W02003016500-A2.
 XX
 XX 27-FEB-2003.
 PF 16-AUG-2002; 2002MO-US026514.
 PR 16-AUG-2001; 2001US-0313080P.
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeiser K;
 PI Allen P;
 DR WPI; 2003-268322/26.
 XX
 PT Determining a toxicological response to an agent, useful for screening of
 PT drugs, comprises comparing the expression profile of one or more human
 PT toxic response genes to a reference gene expression profile indicative of
 PT toxicity.

Claim 1; Page 287; 455pp; English.

CC The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also
 CC described: (1) an array comprising one or more polynucleotides selected
 CC from the genes corresponding to the partial sequences given in AB283764
 CC to AB284764, or their fragments of at least 20 nucleotides, or homologues
 CC; and (2) determining if a gene putatively identified to be a toxic
 CC response gene plays a role on toxic response pathways by determining the
 CC expression profile of the gene after exposure of cells or a human subject
 CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
 CC exposing cells to an agent or isolating cells from a human subject who
 CC was exposed to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals

Sequence 1024 BP; 225 A; 317 C; 263 G; 219 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 18; DB 7; Length 1024;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCACTGGC 18
 DB 206 CCGGAGGCACTGGC 189

RESULT 9

AAZ52304/C
 ID AAZ52304 standard; cDNA, 1070 BP.

AAZ52304;

24-JUL-2000 (first entry)

Human p35 (p53 isoform) cDNA.

Human p53 isoform; p35; marker; hypoxia; myocardial infarction;
 cell proliferation; cytosolic; proliferative; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 136..921

FT /tag= a

PN /product= "Human p35 protein"

WO200022127-A1.

20-APR-2000.

07-OCT-1999; 99WO-US023319.

09-OCT-1998; 98US-0103849P.

(BGM) BRIGHAM & WOMENS HOSPITAL INC.

Del'acqua G, Mann MJ, Deau VJ;

WPI; 2000-117984/27.

P-PSDB; AAY70714.

Novel isoform of p53 useful as a marker of myocardial infarction and for
 controlling cellular proliferation.

Claim 18; Fig 4; 25pp; English.

The present cDNA sequence encodes the human p53 isoform, p35. This p53
 isoform is truncated to eliminate a substantial portion of the C-terminal
 end of the protein. The deleted portion correspond to those encoded by
 CC exon 7 and by exons corresponding to amino acids lying C-terminal to exon
 7. p35 is useful as a marker of myocardial infarction (by the indication
 of hypoxia) and in the control of cell proliferation both in vivo and in
 vitro. It was able to increase the transactivation achieved through co-
 transfection with wild type p53. The combination of p35 with wild type
 CC p53 produce an enhanced inhibition of primary incorporation at 24 hours
 compared to wild type p53 alone

Sequence 1070 BP; 233 A; 338 C; 282 G; 217 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 1070;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCACTGGC 18
 DB 127 CCGGAGGCACTGGC 110

RESULT 10

AA04533/C
 ID AAX04533 standard; DNA, 1303 BP.

AC AAX04533;

13-APR-1999 (first entry)

DNA encoding human p53 protein.

Ataxia telangiectasia; ATM protein; assay; interaction; kinase activity;
 p53; screening; ATR; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 122..1303

FT /tag= a

FT /product= "p53"

GB2327498-A.

27-JAN-1999.

16-JUL-1998; 98GB-00015423.

16-JUL-1997; 97GB-00014971.

(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

Jackson SP, Lakin ND, Smith GCM;

WPI; 1999-073587/07.

P-PSDB; AAW84270.

Assay method for compounds modulating the interaction of ATM and p53 -
 useful for the treatment of e.g. cancer, immunosuppression and HIV
 infections and for the purification of the proteins ATM and ATR.

Disclosure; Fig 7b; 124pp; English.

The present sequence encodes a human p53 protein. The protein is used in
 the assay of the invention. The specification describes an assay method
 for a compound able to modulate the interaction between ATM or a protein
 having an associated kinase activity and p53 or a protein having a
 homologous phosphorylation sites. The assay comprises contacting a
 peptide fragment ATM with a relevant fragment of p53 and a test compound,
 and determining the interaction or binding between the substances and the
 test compound. The assay method is useful for screening for compounds
 able to modulate the interaction between ATM and p53. The screened
 CC agents, peptide fragments and nucleic acids are useful for therapy
 CC involving modulating ATM action e.g. in the treatment of cancer.
 CC immunosuppression or HIV infections by modulating phosphorylation of p53
 by ATM, and for purifying the proteins ATM and ATR

Sequence 1303 BP; 292 A; 403 C; 348 G; 260 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 1303;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCACTGGC 18
 DB 113 CCGGAGGCACTGGC 96

RESULT 11
 AAS73327/C
 ID AAS73327 standard; DNA, 1303 BP.

AB573327;

04-DEC-2002 (first entry)

DNA encoding human oncogene p54.

Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 proliferative disease; cellular protein isoform; heat shock protein 90;

XX	HSP-90; haematoid arthritis; cancer; haematopoietic disorder;
KM	T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KM	acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KM	acute lymphoblastic leukaemia; ALL; APL, NHL, solid tumour;
KM	papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KM	rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
XX	
OS	Homo sapiens.
XX	
XX	WO200269900-A2.
PN	
PD	12-SEP-2002.
XX	
PF	01-MAR-2002; 2002MO-US006518.
XX	
PR	01-MAR-2001; 2001US-0272751P.
PA	(CONF-) CONFORMA THERAPEUTICS CORP.
XX	
PI	Fritz LC, Burrows FT;
XX	
DR	WPI, 2002-698710/75.
DR	P-PDS; ABG95119.
XX	
PT	Treating genetically-defined disease associated with chromosomal
PT	aberrations yielding oncogenic fusion proteins; e.g. cell proliferative
XX	diseases, involves administering an inhibitor of heat shock protein 90.
PS	Disclosure; Page 319-320; 389pp; English.
XX	
CC	The invention describes a method of treating genetically-defined disease
CC	associated with chromosomal aberrations yielding oncogenic fusion
CC	proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC	cell population, treating proliferative diseases associated with mutant
CC	protein or cellular protein isoforms (II) dependent on heat shock protein
CC	(HSP)-90, or selectively treating cells expressing (II) involving
CC	administering HSP90-inhibitor. The method is useful for treating
CC	genetically-defined disease with chromosomal aberration yielding
CC	oncogenic fusion protein, treating cancerous cells containing fusion
CC	protein in heterogeneous cell population, treating proliferative disease
CC	(e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC	cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC	p53), or selectively treating cells expressing mutant protein (HSP)-90
CC	protein isoform in a patient heterozygous for (II). The method is useful
CC	for treating a disease e.g. haematopoietic disorder, such as T or B cell
CC	lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
CC	or a disease characterised by a solid tumour such as papillary thyroid
CC	carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC	synovial sarcoma. The method is also useful for treating viral
CC	infections. This sequence encodes a human oncogenic protein
XX	
XX	
SQ	Sequence 1303 BP; 292 A; 403 C; 348 G; 260 T; 0 U; 0 Other;
	Query Match 100.0%; Score 18; DB 6; Length 1303;
	Best Local Similarity 100.0%; Pred. No. 28;
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 CCCGAGAGCAGCTCGAC 18
DB	113 CCCGAGAGCAGCTCTGC 96
RESULT 12	
ID	ACC49400/c
XX	ACC49400 standard; cDNA; 1303 BP.
AC	ACC49400;
XX	
DT	24-JUN-2003 (first entry)
XX	
DS	Human p53 encoding cDNA.
XX	
KM	Human; ATM; p53; ATR; FRP1; FRAP related protein; DNA-PK; DNA-PKcs;

	OS	Homo sapiens.	
	XX		
	XX	Key	Location/Qualifiers
	PH	CDS	122..1303
	FT	/tag= a	
	FT	/product= "p53"	
	FT	/transl_except= {pos:1232, 1234;aa:Ser}	
	FT	/note= "Illegible parts of the nucleotide sequence in the figure"	
	FN		
	PX	GB2362952-A.	
	PD	05-DEC-2001.	
	PD		
	PF	21-AUG-2001; 2001GB-00020368.	
	PX		
	PR	16-JUL-1997; 97GB-00014971.	
	PX	16-JUL-1998; 98GB-00015423.	
	PA	(KUDO-) KUDOS PHARM LTD.	
	PX		
	PI	Jackson SP, Lakin ND, Smith GCM;	
	DR	NPL; 2003-2232383/23.	
	DR	p-psDB; ABP97119.	
	PX		
	PT	Assay for compound affecting DNA binding by ataxia-telangiectasia mutated gene, by bringing into contact the gene, protein with kinase activity,	
	PT	DNA and test compound, and determining binding of the gene and DNA.	
	PX		
	PS	Disclosure; Fig 7bi-ii; 129pp; English.	
	XX		
	CC	The present invention describes an assay (M1) for a compound able to affect DNA binding by an ataxia-telangiectasia mutated (ATM) protein or a protein having an associated kinase activity. M1 comprises bringing into contact a substance which is ATM or a protein having an associated kinase activity which is able to bind DNA and a test compound, and determining binding of ATM and DNA in the presence of the test compound. Also described: (I) an agent (I) capable of affecting DNA binding by ATM obtained using M1; (2) purifying (M2) ATM or related kinase such as ATR; (3) use of DNA (II) for purifying ATM or ATR; and (4) a substantially pure ATM (III) or ATR (IV). ATM has anti-HIV, cytostatic, antiproliferative and antitumour activities. M1 is useful for assaying for a compound able to affect DNA binding by ATM or a protein having an associated kinase activity. (I) is useful in therapy involving modulating ATM action or in the manufacture of a medicament for modulating ATM action. (II) is useful for purifying ATM or ATR. (I) is also useful for treating humans with ataxia-telangiectasia, AIDS or cancer, for treating or preventing disease states associated with premature and normal aging for regulating immune system function, for inhibiting cell proliferation by activating cell cycle check point arrest in the absence of cellular damage, which may be used in the treatment of tumours, cancer, psoriasis and other hyperproliferative disorders, for activating p53 in cells without damaging the cells, for augmenting cancer radiotherapy and chemotherapy, or as adjuvants in cancer radiotherapy and chemotherapy. The present sequence encodes human p53 which is given in the exemplification of the present invention	
	SC		
SQ	Sequence	1303 BP; 289 A; 401 C; 344 G; 257 T; 0 U; 12 Other;	
EY	Query Match	100.0%; Score 18; DB 7; Length 1303;	
	Best Local Similarity	100.0%; Pred. No. 28;	
	Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
db	113 CCCTGAAGGCACTTCGGC 96		

```
RESULT 13
AAD00088/c
ID AAD00088 standard; DNA; 1307 BP.
XX
XX AAD00088;
AC
XX 31-JUL-2000 (first entry)
DT
XX Human tumour-associated antigen p53 DNA.
DE
XX Human; tumour-associated antigen; p53 protein; DNA-binding domain;
KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
KW SLE; systemic lupus erythematosus; diagnosis; treatment; prevention; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 126..1307
FT CDS /*tag= a
FT /product= "p53 protein"
XX
XX WO20023082-A1.
XX
XX 27-APR-2000.
XX
XX 19-OCT-1999; 99WO-US024443.
XX
XX 19-OCT-1998; 98US-0104816P.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Cohen IR, Rotter V, Erez-Alon N, Herkel J;
XX WPI; 2000-339512/29.
XX P-PSDB; AAY70811.
XX
XX Treatment of systemic lupus erythematosus by down-regulating the
PT autoimmune response to the C-terminal DNA-binding domain of the p53
PT protein by an active compound comprising of antibodies to p53 or
PT fragments of p53.
XX
XX Disclosure: Page 79-81; 87pp; English.
XX
XX The patent discloses a method for the treatment of systemic lupus
XX erythematosus (SLE) by down-regulating the autoimmune response to the C-
XX terminal DNA-binding domain of p53 protein by an active compound
XX comprising C-terminal DNA-binding domain of p53, monoclonal antibodies
XX (Ab1) specific to this domain, monoclonal antibodies (Ab2) specific to
XX Ab1 and peptides based on the complementarity determining region of heavy
XX and light chain of Ab1 and Ab2. The active compound is useful in the
XX diagnosis, prevention and treatment of SLE in humans. The present
XX sequence is a human tumour-associated antigen p53 DNA. Antibodies against
XX the C-terminal DNA-binding domain of the p53 protein can be raised and
XX used for diagnosis and treatment of SLE.
XX
SQ Sequence 1307 BP; 293 A; 404 C; 350 G; 260 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 3; Length 1307;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGAGAGCAGTCTGGC 18
DB 117 CCCGAGAGCAGTCTGGC 100
RESULT 14
ABX15394/c
ID ABX15394 standard; DNA; 1307 BP.
XX
XX ABX15394;
AC
XX 01-MAY-2003 (first entry)
DT
```

```
XX
XX Human p53 DNA.
DE
XX Human; p53; degradation; cervical cancer; tumour; ovarian cancer; glioma;
KW carcinoma; squamous cell carcinoma; lung cancer; pancreatic cancer;
KW leukaemia; lymphoma; neuroblastoma; sarcoma; osteosarcoma; glioblastoma;
KW colon carcinoma; melanoma; choriocarcinoma; breast carcinoma; gene; ds;
KW neuroblastoma; rhabdomyosarcoma; Mdm2; cytostatic; antitumour.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 126..1307
FT CDS /*tag= a
FT /product= "Human p53"
XX
XX US2002132977-A1.
XX
XX 19-SEP-2002.
XX
XX 07-DEC-2000; 2000US-00732384.
XX
XX 08-DEC-1999; 99US-0169816P.
XX
XX (YUAN/) YUAN Z.
XX (GUJ/) GU J.
XX
XX Yuan Z, Gu J;
XX WPI; 2003-197937/19.
XX P-PSDB; AEG73431.
XX
XX Novel polypeptide that inhibits degradation of endogenous p53 in a
PT mammalian cell, useful for treating cancer, e.g. cervical cancer or a
PT tumor such as sarcoma or carcinoma.
XX
XX Example 2; Page 3; 21pp; English.
XX
XX The invention relates to a substantially pure polypeptide that inhibits
XX degradation of endogenous p53 in a mammalian cell. The polypeptide or a
XX synthetic polypeptide comprising a region of the pure polypeptide is
XX useful for inhibiting degradation of endogenous p53 in a mammalian cell,
XX e.g. in cervical cancer cells or tumour cells selected from sarcoma,
XX carcinoma, squamous cell carcinoma, ovarian cancer, lung cancer,
XX pancreatic cancer, leukaemia, lymphoma, glioma, neuroblastoma,
XX osteosarcoma, colon carcinoma, melanoma, choriocarcinoma, breast
XX carcinoma, glioblastoma, neuroblastoma and rhabdomyosarcoma cells. The
XX cell comprises an Mdm2 amplification or overexpresses Mdm2. A degradation
XX -resistant p53 polypeptide is useful for inhibiting tumour growth, where
XX the tumour is a cervical cancer and comprises a p53 mutation. The
XX polypeptide, and DNA encoding the polypeptide, are useful for treating
XX cancer. This sequence represents DNA encoding the human p53 polypeptide
XX
SQ Sequence 1307 BP; 293 A; 404 C; 350 G; 260 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 7; Length 1307;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGAGAGCAGTCTGGC 18
DB 117 CCCGAGAGCAGTCTGGC 100
RESULT 15
AAT32831/c
ID AAT32831 standard; DNA; 1317 BP.
XX
XX AAT32831;
AC
XX 06-NOV-1996 (first entry)
DT Human p53 tumour suppressor protein gene.
DE
```

```

XX p53 protein; tumour suppressor; tetramerisation domain;
XX chimaeric protein; gene therapy; vector; cell proliferation; cancer;
XX apoptosis; autoimmune disease; immune tolerance; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 136..1317
FT /*tag= a
XX
XX MO9616989-A1.
XX
XX 06-JUN-1996.
XX
XX 27-NOV-1995; 95WO-US015353.
XX
XX 28-NOV-1994; 94US-00347792.
XX 28-APR-1995; 95US-00431357.
XX 01-JUN-1995; 95US-00456623.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Halazonetis TD;
XX
XX WPI; 1996-286828/29.
XX P-PSDB; AAM02617.
XX
XX New chimaeric p53 protein with heterologous tetramerisation domain - and
XX related DNA and vectors, useful for treating abnormal cell proliferation,
XX esp. cancer, auto-immune disease, etc.
XX
XX Disclosure; Page 66-68; 123pp; English.
XX
XX A DNA sequence (AA12831) codes for wild-type p53 protein (AAM02617), a
XX sequence-specific DNA binding protein which has tumour suppressor
XX function. p53 regulates cell proliferation and apoptosis and participates
XX in cellular response to DNA damaging agents. It is inactivated in more
XX than half of all human tumours. DNA constructs encoding p53 proteins with
XX altered tetramerisation domains that retain wild-type p53 function can be
XX used in gene therapy to treat abnormal cell proliferation, esp. cancer.
XX or to induce immune tolerance to facilitate transplants and treat
XX autoimmune diseases
XX
XX Sequence 1317 BP; 297 A; 408 C; 350 G; 262 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 18; DB 2; Length 1317;
XX Best Local Similarity 100.0%; Pred. No. 28;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCGGAAGGCGAGTCTGGC 18
DB 127 CCCGGAAGGCGAGTCTGGC 110
XX
XX RESULT 16
XX AAV18151/c
XX ID AAV18151 standard; DNA; 1317 BP.
XX
XX AAV18151;
XX
XX 21-AUG-1998 (first entry)
XX
XX Nucleotide sequence of human p53 gene.
XX
XX Human p53 gene; vaccine; chemokine; cytokine; immune response; tumour;
XX mutation; antigen; cancer; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 136..1317
XX /*tag= a
FT

```

```

FT /product= "human p53"
XX
XX MO9815285-A1.
XX
XX 16-APR-1998.
XX
XX 10-OCT-1997; 97WO-US018807.
XX
XX 10-OCT-1996; 96US-0028193P.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Ert1 HCU, Thurin M;
XX
XX WPI; 1998-240594/21.
XX P-PSDB; AAM46858.
XX
XX Pharmaceutical or vaccine comprising DNA encoding p53 and optionally
XX chemokine or cytokine - is useful for treatment and prevention of tumours
XX by inducing protective immune response.
XX
XX Disclosure; Page 51-53; 74pp; English.
XX
XX This is the nucleotide sequence of the human p53 gene, used in the method
XX of the invention involving a pharmaceutical or vaccine comprising DNA
XX encoding p53 and optionally a chemokine or cytokine. The compositions and
XX methods can be used for inducing immune responses to tumour cells which
XX over-express p53 or express mutated p53. They can be used to induce a
XX response to tumour antigens to cause a regression of existing tumours
XX and/or prevent the development of cancers, in e.g. high risk patients
XX
XX Sequence 1317 BP; 297 A; 408 C; 350 G; 262 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 18; DB 2; Length 1317;
XX Best Local Similarity 100.0%; Pred. No. 28;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCGGAAGGCGAGTCTGGC 18
DB 127 CCCGGAAGGCGAGTCTGGC 110
XX
XX RESULT 17
XX AAV21414/c
XX ID AAV21414 standard; DNA; 1317 BP.
XX
XX AAV21414;
XX
XX 04-AUG-1998 (first entry)
XX
XX Human p53 cDNA homologous probe 3.
XX
XX Probe; gene mapping; RecA-like recombinase; human p53; lambda phage;
XX in situ hybridisation; infectious disease; gene therapy; ds.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9808975-A1.
XX
XX 05-MAR-1998.
XX
XX 29-AUG-1997; 97WO-JF003019.
XX
XX 29-AUG-1996; 96JP-00229061.
XX 26-DEC-1996; 96JP-00347090.
XX
XX (DAIK ) DAIKIN IND LTD.
XX
XX Kigawa K, Yamanaka M, Kusumi K, Mukai E, Ohta K;
XX WPI; 1998-179448/16.
XX

```

PT Targeting DNA by reaction with homologous probe and recombinase - with
 PT addition of heterologous probe to increase efficiency and sensitivity,
 PT useful for in situ hybridisation, gene therapy, cloning of genes, gene
 PT mapping etc.
 XX
 XX
 XX Example 1; Page 44; 59pp; English.
 CC The invention provides a method for detecting target DNA in a sample
 CC using RecA-like recombinase and probes homologous to the target DNA.
 CC Addition of heterologous probes was found to increase the sensitivity and
 CC efficiency of detecting the target DNA. In the example given, the target
 CC DNA was the human p53 cDNA which was incorporated in a pHP53B plasmid.
 CC Homologous probes 1-6 (AAV21407, AAV21408, AAV21412, AAV21414-V21416)
 CC containing a partial sequence of the p53 cDNA were used. The heterologous
 CC probes 1-4 (AAV21409-V21411 and AAV21413) corresponded to a partial
 CC sequence of the lambda phage genome. To measure the specificity of
 CC detecting the target DNA, a heterologous double stranded circular DNA
 CC (plasmid vector pUC18) was also used. The method is useful for detecting
 CC the target DNA in cells by in situ hybridisation and to target the DNA in
 CC living cells by in vivo gene targeting, e.g. for gene therapy. The method
 CC is also claimed to be useful for isolating and cloning target genes from
 CC libraries, in gene mapping and for detecting genetic aberrations or
 CC mutations or infectious diseases
 XX
 XX Sequence 1317 BP; 293 A; 407 C; 359 G; 258 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 18; DB 2; Length 1317;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGGAGGAGGAGTCTGGC 18
 Db 187 CCGGAGGAGGAGTCTGGC 170
 RESULT 18
 AAV44695/C
 ID AAV44695 standard; DNA; 1317 BP.
 AC AAV44695;
 XX
 XX 19-OCT-1998 (first entry)
 DT
 XX
 DE Human wild-type p53 protein encoding DNA.
 XX
 XX Hydrophobic; p53 protein; mutant; oligomerisation domain; dimerisation;
 KW therapeutic agent; biotechnology; tumour suppressor; apoptosis; human;
 KW transplant rejection; autoimmune disease; systemic lupus erythematosus;
 KW rheumatoid arthritis; psoriasis; atherosclerosis; arterial restenosis;
 KW abnormal cell proliferation; interleukin-2 receptor complex;
 KW three-dimensional structure; 3D structure; transmembrane receptor; ds.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT 136..1317
 FT CDS /tag= a
 FT /product= "wild-type p53 protein"
 PN
 XX WO9831703-A1.
 XX
 XX 23-JUL-1998.
 PD
 XX 15-JAN-1998; 98WO-US000853.
 PF
 XX 17-JAN-1997; 97US-0035458P.
 PR
 XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 PA
 XX Halazonectis TD;
 PI
 XX WPI; 1998-414033/35.
 DR P-PSDB; AAW69217.

XX
 PT Altering three-dimensional structure of protein without denaturing it -
 PT by replacing large hydrophobic amino acids with small ones, or vice
 PT versa, used to, e.g. produce p53 proteins with altered oligomerisation
 PT properties.
 XX
 XX
 XX Example 1; Page 33-34; 49pp; English.
 CC This DNA encodes a wild-type p53 protein. The invention provides a method
 CC for altering the three-dimensional (3D) structure of a protein, without
 CC denaturing the protein. The method comprises identifying hydrophobic
 CC residues in the protein and classifying the residues as large or small
 CC according to size of the side chain. Mutants in which the hydrophobic
 CC residues have been substituted are produced and they can be analysed for
 CC a change in the 3D structure. The method is applied to non-linear
 CC proteins having a hydrophobic core. A p53 oligomerisation domain can be
 CC altered by this method. Vectors containing nucleic acids encoding a p53
 CC oligomerisation domain and fusion proteins of the p53 oligomerisation
 CC domain with a heterologous domain are useful as therapeutic and
 CC diagnostic agents, in biotechnology and other industrial applications.
 CC Typically altered p53 is useful as tumour suppressor, to induce apoptosis
 CC in proliferating lymphocytes, to prevent transplant rejection, to treat
 CC autoimmune diseases such as systemic lupus erythematosus and rheumatoid
 CC arthritis, and to suppress proliferation in cases of psoriasis,
 CC atherosclerosis and arterial restenosis. They are also used to diagnose
 CC diseases associated with p53 and abnormal cell proliferation. Typical
 CC heterologous proteins are antibodies against Fos or Jun, soluble
 CC interleukin-2 receptor complex (for screening drugs that bind the native
 CC receptor and as therapeutic decoys) and transmembrane receptors. The p53
 CC oligomerisation domain may also be used to induce dimerisation of DNA-
 CC binding proteins, especially c-myc. Altered proteins retain biological
 CC function but have better stability, binding and lower molecular weight
 CC (so enter cells more easily). When expressed from a gene therapy vector,
 CC the altered p53 will not be sequestered into inactive heterodimers by
 CC mutant p53 present in the cells
 XX
 XX Sequence 1317 BP; 297 A; 408 C; 350 G; 262 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 18; DB 2; Length 1317;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGGAGGAGGAGTCTGGC 18
 Db 127 CCGGAGGAGGAGTCTGGC 110
 RESULT 19
 AAC84597/C
 ID AAC84597 standard; DNA; 1317 BP.
 AC AAC84597;
 XX
 XX 02-APR-2001 (first entry)
 DT
 XX
 DE Human p53 protein encoding DNA.
 XX
 XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
 KW CUL-1; cullin; CDC63; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytoskeletal; ds.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200075184-A1.
 PN
 XX 14-DEC-2000.
 PD
 XX 05-JUN-2000; 2000WO-US015449.
 PF
 XX 04-JUN-1999; 99US-0137494P.
 PR
 XX (UYVA) UNIV YALE.
 PA
 XX

Query Match	100.0%	Score 18;	DB 4;	Length 1317;
Best Local Similarity	100.0%;	Pred. No. 28;		
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1	CCCCGAAGCAGCTGTCG	18	
Db	127	CCCCGAAGCAGCTGTCG	110	
RESULT 20				
AAD12279/c				
ID	AAD12279	standard;	CDNA;	1317 BP.
XX				
AC	AAD12279;			
XX				
XX	25-SEP-2001	(first entry)		
DT				
XX				
XX	Human p53 cDNA.			
DE				
XX				
KM	Human; gene structure; phenotypic expression; guanosine cofactor;			
KM	gemline variation analysis; exon-intron boundary; tetrahymena rRNA; p53;			
XX	ss.			
OS	Homo sapiens.			
XX				
XX				
PH	Key	Location/Qualifiers		
FT	primer_bind	complement(46..66)		
FT		/*tag= a		
FT		/bound_molety= "Primer 1a"		
FT		136..138		
FT	misc_signal	/*tag= b		
FT		/note= "Translation start site"		
FT	primer_bind	complement(137..156)		
FT		/*tag= c		
FT		/bound_molety= "Primer 2a"		
FT	primer_bind	complement(321..344)		
FT		/*tag= d		
FT		/bound_molety= "Primer 3a"		
FT		complement(516..535)		
FT		/*tag= e		
FT	primer_bind	/bound_molety= "Primer 4a"		
FT		complement(615..634)		
FT		/*tag= f		
FT	primer_bind	/bound_molety= "Primer 5a"		
FT		640..659		
FT		/*tag= g		
FT	primer_bind	/bound_molety= "Primer 5b"		
FT		complement(792..811)		
FT		/*tag= h		
FT	primer_bind	/bound_molety= "Primer 6a"		
FT				

```

FT primer_bind complement(933. .952)
FT /tag= i
FT /bound_moiety= "Primer 7a"
FT primer_bind 962. .981
FT /tag= j
FT /bound_moiety= "Primer 7b"
FT primer_bind 1082. .1101
FT /tag= k
FT /bound_moiety= "Primer 8b"
FT primer_bind complement(1124. .1143)
FT /tag= l
FT /bound_moiety= "Primer 8a"
FT primer_bind complement(1257. .1276)
FT /tag= m
FT /bound_moiety= "Primer 9a"
FT
FT
FT WO200153529-A2.
FT
FT 26-JUL-2001.
FT
FT 17-JAN-2001, 2001WO-US001461.
FT
FT 20-JAN-2000, 2000US-00488127.
FT
FT (GENO-) GENOME THERAPEUTICS CORP.
FT
FT Thomann H, Filtzgerald MS;
FT
FT WPI; 2001-465380/50.
FT
FT Determining structure of genes whose sequence is not known from cDNA, by
FT sequencing the gene or gene across exon-intron boundaries using evenly
FT spaced primers comprising nucleic acids that hybridize to the cDNA of
FT gene.
FT
FT Example 2; Fig 2; 81pp; English.
FT
FT The present invention relates to a method for determining gene structure
FT when the genomic sequence is unknown. The method involves sequencing the
FT gene across exon-intron boundaries using evenly spaced primers or tiled
FT primers. The tiled primers comprises nucleic acids that hybridizes to the
FT known cDNA sequence of the gene at about 100-300 base intervals and the
FT gene comprises the template. Gene structure can be determined without the
FT need to sequence the entire gene. The method provides information
FT necessary to determine gene structure and phenotypic expression without
FT the need to sequence entire chromosomal copy of the gene or fragment. The
FT methods are useful in germline sequence variation analysis. The method is
FT also useful for determining the boundaries between regions of nucleic
FT acids that were separated by intervening sequence, and also for
FT determining boundaries present in genes containing group 1 type introns
FT such as Tetrahymena rRNA, where self-splicing occurs in the presence of
FT guanosine cofactor. The present sequence is human p53 cDNA related to the
FT invention
FT
FT Sequence 1317 BP; 295 A; 408 C; 352 G; 262 T; 0 U; 0 Other;
FT
FT Query Match 100.0%; Score 18; DB 4; Length 1317;
FT Best Local Similarity 100.0%; Pred. NO. 28;
FT Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT 1 CCCGGAAGGCAAGTCTGGC 18
FT |||||
FT 127 CCCGGAAGGCAAGTCTGGC 110
FT
FT RESULT 21
FT AAD43929/c
FT ID AAD43929 standard; DNA; 1317 BP.
FT
FT AC AAD43929;
FT
FT 13-DEC-2002 (first entry)
FT

```


DE Human p53 wild-type DNA.
 XX
 KW Human; p53 protein; transplant rejection; systemic lupus erythematosus;
 KW autoimmune disease; rheumatoid arthritis; atherosclerosis; psoriasis;
 KW cancer; arterial restenosis; vaccine; gene therapy; protein therapy;
 KW immunosuppressant; cytostatic; antiatherosclerotic; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 136. 1317
 FT CDS /*tag= a
 FT /product= "Human p53 wild-type protein"
 FT
 XX US638062-B1.
 XX
 XX 14-MAY-2002.
 XX
 XX PD 05-MAY-1999; 99US-00305914.
 XX
 XX PF 08-MAY-1998; 98US-0084839P.
 XX
 XX PR (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX
 XX PA Halazonetis TD, Stavridi ES;
 XX
 XX PI WPI: 2002-462356/49.
 XX
 XX DR P-PSDB; AAE26342.
 XX
 XX PT Modified p53 protein useful for preventing diagnosing and treating e.g.
 PT cancers and psoriasis, comprises a modified p53 tetramerization domain
 PT that does not hetero-oligomerize with the native p53 tetramerization
 PT domain.
 XX
 XX PS Disclosure: Col 13-16; 14pp; English.
 XX
 XX CC The present invention relates to novel modified p53 proteins containing a
 CC p53 DNA binding domain and a modified p53 tetramerization domain that
 CC does not hetero-oligomerize with the native p53 tetramerization domain.
 CC Sequences of the invention are useful for the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate p53 expression and
 CC activity. They are used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of p53 by expressing inactive proteins or to
 CC supplement the patient's own production of p53. p53 sequences are useful
 CC to prevent transplant rejection, to treat autoimmune diseases such as
 CC systemic lupus erythematosus, rheumatoid arthritis, cancers, psoriasis,
 CC atherosclerosis and arterial restenosis. They are also used as vaccines.
 CC Sequences of the invention are used in gene therapy and protein therapy.
 CC The present sequence is human p53 wild-type DNA
 CC
 XX SQ Sequence 1317 BP; 297 A; 408 C; 350 G; 262 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 18; DB 6; Length 1317;
 XX Best Local Similarity 100.0%; Pred. No. 28;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCGAGGCGAGCTGTGGC 18
 DB 127 CCCGAGGCGAGCTGTGGC 110
 RESULT 22
 ID AAT79880/c
 XX AAT79880 standard; DNA; 1760 BP.
 AC AAT79880;
 XX
 XX 03-DEC-1997 (first entry)
 DT
 XX DNA encoding human p53 variant found in bone marrow cell line CMC-1.
 DE
 XX Bone marrow; acute myelocytic leukaemia; p53 mutant; chromosome (8);
 KW

KW 12) locus; 17th chromosome deficient; myeloperoxidase production;
 KW antifungal; antiviral; ss.
 XX
 XX OS Homo sapiens.
 XX
 XX FH Key Location/Qualifiers
 XX CDS 215. .1396
 XX
 XX FT /*tag= a
 XX FT 539. .541
 XX FT /*tag= b
 XX FT /note= "TTV to TTG mutation resulting in Phe to Leu
 XX mutation in resultant protein"
 XX FT 936. .938
 XX FT /*tag= c
 XX FT /note= "CGG to CAG mutation resulting in Arg to Gln
 XX mutation in resultant protein"
 XX FT 1031. .1033
 XX FT /*tag= d
 XX FT /note= "CGT to CATT mutation resulting in Arg to His
 XX mutation in resultant protein"
 XX FT 1316. .1318
 XX FT /*tag= e
 XX FT /note= "CAC to CGC mutation resulting in His to Arg
 XX mutation in resultant protein"
 XX
 XX PV JP09206070-A.
 XX
 XX PD 12-AUG-1997.
 XX
 XX PF 31-JAN-1996; 96JP-00037400.
 XX
 XX PR 31-JAN-1996; 96JP-00037400.
 XX
 XX PA (SRLS-) SRL KK.
 XX
 XX DR WPI: 1997-460745/43.
 XX
 XX DR P-PSDB; AAW25155.
 XX
 XX PT Cell line derived from leukaemic human bone marrow cells - used for the
 PT production of myeloperoxidase which has antifungal and antiviral
 PT activity.
 XX
 XX PS Disclosure; Page 4-6; 6pp; Japanese.
 XX
 XX CC AAT79880 is a DNA sequence encoding a p53 mutant protein. The DNA can be
 CC found in a new cell line CMC-1 (FERM P-1507), which was derived from a
 CC bone marrow cell of a patient with acute myelocytic leukaemia. The cell
 CC line has the following characteristics: (a) a chromosomal (8; 21) locus;
 CC (b) is deficient in one of 17th chromosomes; and (c) has mis-sense
 CC mutations on codons 248 and 368 of the p53 gene. The features table shows
 CC these mutations as tags c and e. Mutations shown by tags b and d are not
 CC explained in the specification. The cell line is used for production of
 CC myeloperoxidase (MPO) which has anti-fungal and anti-viral activity or as
 CC a control for detection of the (8; 21) locus in studying acute bone
 CC marrow leukemia. MPO can be supplied in a large amount as opposed to
 CC conventional production of MPO from blood as the starting material
 CC
 XX SQ Sequence 1760 BP; 401 A; 512 C; 461 G; 386 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 18; DB 2; Length 1760;
 XX Best Local Similarity 100.0%; Pred. No. 28;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCGAGGCGAGCTGTGGC 18
 DB 206 CCCGAGGCGAGCTGTGGC 189
 RESULT 23
 ID AAX75765/c
 XX AAX75765 standard; DNA; 1760 BP.
 AC AAX75765;
 XX

XX 22-JUL-1999 (first entry)
 DT
 XX
 DE Human p53 cellular tumour antigen DNA.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin 1; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A; ss.

OS Homo sapiens.

XX WO9845322-A2.

XX 15-OCT-1998.

XX 02-APR-1998; 98WO-IB000705.

XX 10-APR-1997; 97US-0043163P.

XX (ROYA-) ROYAL NETHERLANDS ACADEMY OF SCI.

XX (UYRO-) UNIV ROTTERDAM ERASMUS.

XX (UYUT-) RIKSUNIV UTRECHT.

XX Van Leeuwen FM, Grosveld FG, Burbach JPH,

XX WPI; 1998-609901/51.

PT Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also for
 PT treatment and prevention with specific ribozymes or wild-type RNA.

XX Disclosure; Fig 14; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease, II
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins tau and Big tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A. This sequence
 CC encodes the wild type and mutant protein fragments represented in
 CC AY21054-Y21103

XX Sequence 1760 BP; 401 A; 513 C; 460 G; 386 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 2; Length 1760;

XX Best Local Similarity 100.0%; Pred. No. 28;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 CCCGGAAGCAGTCTGGC 18

DB 206 CCCGGAAGCAGTCTGGC 189

RESULT 24

AA054029/c

AD AAD54029;

DT 17-JUN-2003 (first entry)

DE Human colon cancer-associated polypeptide gene, CO-13 (P53).

XX Human; colon cancer-associated polypeptide; immune response; therapy;

XX colon cancer; gene; ds.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX CDS 215..1273

XX /tag= a

XX /product= "Human colon cancer-associated polypeptide"

XX /transl_except= (pos:440..442, aa:Xaa)

XX /transl_except= (pos:502..505, aa:Val)

XX /note= "Xaa corresponds to any amino acid"

XX WO200290986-A1.

XX 14-NOV-2002.

XX 02-MAY-2002; 2002WO-US013994.

XX 04-MAY-2001; 2001US-00849602.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (CORR) CORNBELL RES FOUNDR INC.

XX Chen Y, Old LJ, Scanlan MJ, Stockert E,

XX WPI; 2003-112003/10.

XX P-PSDB; AAE35350.

XX Diagnosing colon cancer in a subject comprises identifying colon cancer-

XX associated polypeptides as antigens that elicit immune response in colon

XX cancer.

XX Claim 1; Page 83-84; 122pp; English.

XX The invention relates to a method for diagnosing colon cancer in a

XX subject which comprises identifying colon cancer-associated polypeptides

XX as antigens that elicit immune response in colon cancer. The method is

XX useful for diagnosing, determining onset, progression, or regression of

XX colon cancer in a subject, or for selecting a course of treatment of a

XX subject having or suspected of having colon cancer. The colon cancer-

XX associated polypeptides are useful as markers for diagnosing colon

XX cancer, and for following the course of treatment of colon cancer. The

XX present sequence is human colon cancer-associated polypeptide gene

XX Sequence 1760 BP; 400 A; 513 C; 461 G; 386 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 7; Length 1760;

XX Best Local Similarity 100.0%; Pred. No. 28;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 CCCGGAAGCAGTCTGGC 18

DB 206 CCCGGAAGCAGTCTGGC 189

RESULT 25

ABA00952/c

AD ABA00952;

DT 16-MAY-2003 (first entry)

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XX DE Human p53 ORF and surrounding sequences.
XX XX
XX KW Gene; screening; silent information regulator 2; Sir2; deacetylation;
XX KW transcription factor; modulator; p53; DNA repair; apoptosis; oncogenesis;
XX KW gene silencing; senescence; cancer; aging; ionizing radiation; ss.
XX OS
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 215..1396
XX FT /*tag=a
XX FT /product="p53"
XX PN WO2003004621-A2.
XX PD 16-JAN-2003.
XX XX
XX PF 08-JUL-2002; 2002MO-US021461.
XX XX
XX PR 06-JUL-2001; 2001US-0303370P.
XX PR 06-JUL-2001; 2001US-0303456P.
XX PR 05-JUL-2002; 2002US-00303456.
XX XX
XX PA (ELIX-) ELIXIR PHARM INC.
XX PI Guarente L, Vaziri H, Imai S, Gu W,
XX WPI; 2003-210354/20.
XX DR P-PSDB; AAG79917.
XX XX
XX PT Screening for modulators of silent information regulator 2 (Sir2) protein
XX PT for treating cancer and aging, comprises determining if the compound
XX PT modulates Sir2-mediated deacetylation of the transcription factor.
XX XX
XX PS Disclosure; Fig 14; 93pp; English.
XX XX
XX CC The sequences given in ABA00951-59 encode proteins which were used in the
XX CC method of the invention for the screening of a compound. The method
XX CC comprises determining if the compound modulates silent information
XX CC regulator 2 (Sir2) interaction with a transcription factor or Sir2-
XX CC mediated deacetylation of a transcription factor in a reaction mixture
XX CC comprising Sir2, a transcription factor and the compound. The method is
XX CC useful for screening compounds that modulate cellular and organismal
XX CC processes. Modulators of Sir2 and/or p53 activity are useful in
XX CC modulating various cellular processes, e.g. repair of DNA damage,
XX CC apoptosis, oncogenesis, gene silencing and senescence. Such modulators
XX CC are also useful for treating cancer and aging, or for treating a cell
XX CC that has been exposed to ionizing radiation
XX CC
XX SQ Sequence 1760 BP; 401 A; 513 C; 460 G; 386 T; 0 U; 0 Other;

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Query Match 100.0%; Score 18; DB 7; Length 1760;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCCGAGAGGCACTGTGCG 18
DB 206 CCCGAGAGGCACTGTGCG 189

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RESULT 26
ADD22450/c
ID ADD22450 standard; DNA; 2451 BP.
XX
XX AC ADD22450;
XX XX
XX DT 15-JAN-2004 (first entry)
XX XX
XX DE HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ No 100.
XX KW tumour antigenic peptide; cancer; vaccine; cytostatic; cytotoxic T cell;
XX KW colon; mouth; lung; prostatic; gynecological; human; gene; ds.

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XX OS Homo sapiens.
XX XX
XX PN JP2003111595-A.
XX XX
XX PD 15-APR-2003.
XX XX
XX PF 24-JUN-2002; 2002JP-00183603.
XX XX
XX PR 25-JUN-2001; 2001JP-00191974.
XX XX
XX PA (ITOY) ITO Y.
XX XX
XX DR WPI; 2003-611129/58.
XX XX
XX PT Novel tumor antigenic peptide or polypeptide useful for inducing
XX PT cytotoxic T cells or for treating cancer such as colon, mouth, lung,
XX PT prostatic or gynecological cancer.
XX XX
XX PS Claim 10; SEQ ID NO 100; 98pp; Japanese.
XX XX
XX CC The invention relates to a novel tumor antigenic peptide or polypeptide
XX CC comprising a sequence selected from 99 sequences fully defined in the
XX CC specification. The tumour antigenic peptide or polypeptide comprises a
XX CC sequence selected from 99 sequences fully defined in the specification,
XX CC where the tumour antigenic peptide preferably has a sequence of Glu-Pro-
XX CC Pro-Leu-Ser-Gln-Glu-Tyr-Phe, and the polypeptide preferably has a
XX CC sequence comprising 393 amino acids fully defined in the specification.
XX CC The invention further provides a cancer vaccine comprising a tumour
XX CC antigenic peptide or polypeptide, which has cytostatic activity. A tumour
XX CC antigenic peptide, polypeptide, its encoding polynucleotide, a
XX CC hybridising polynucleotide, a recombinant vector containing the
XX CC polynucleotide, a host transformed with the vector or an antibody are
XX CC useful for screening for compounds that interact with the tumour
XX CC antigenic peptide, the polypeptide or its encoding polynucleotide and
XX CC increases the expression of the tumour antigenic peptide, the polypeptide
XX CC or polynucleotide. The tumour antigenic peptide or the polypeptide is
XX CC useful for inducing cytotoxic T cells. The tumour antigenic peptide
XX CC vaccine is useful for treating cancer such as colon, mouth, lung,
XX CC prostatic or gynecological cancer. The invention also provides a
XX CC pharmaceutical composition useful for treating cancer. The tumour
XX CC antigenic peptide or the polypeptide is useful as an antigen to create
XX CC antibodies. This polynucleotide sequence represents the DNA encoding one
XX CC of the human tumour antigenic polypeptides of the invention.
XX XX
XX SQ Sequence 2451 BP; 537 A; 697 C; 592 G; 625 T; 0 U; 0 Other;

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Query Match 100.0%; Score 18; DB 9; Length 2451;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCCGAGAGGCACTGTGCG 18
DB 55 CCCGAGAGGCACTGTGCG 38

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RESULT 27
AAS65699/c
ID AAS65699 standard; cDNA; 2600 BP.
XX
XX AC AAS65699;
XX XX
XX DT 13-FEB-2002 (first entry)
XX XX
XX DE DNA encoding novel human diagnostic protein #1503.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX XX
XX OS Homo sapiens.
XX KW WO200175067-A2.

```

PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Dmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR P-PSDB; ABG01512.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 1; SEQ ID NO 1503; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 2600 BP; 562 A; 741 C; 641 G; 656 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 5; Length 2600;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCAAGTCTGGC 18
DB 206 CCCGGAAGGCAAGTCTGGC 189

RESULT 28
AAS67409/C

ID AAS67409 standard; cDNA; 2605 BP.

XX AAS67409;

DT 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #3213.

XX Human; chromosome mapping; gene mapping; gene therapy; forensics;

XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Dmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR P-PSDB; ABG03222.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 1; SEQ ID NO 3213; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 2605 BP; 558 A; 740 C; 644 G; 663 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 5; Length 2605;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCAAGTCTGGC 18
DB 206 CCCGGAAGGCAAGTCTGGC 189

RESULT 29
ABA09379/C

ID ABA09379 standard; cDNA; 397 BP.

XX ABA09379;

DT 11-JAN-2002 (first entry)

XX Human p53 homologue-encoding cDNA, SEQ ID NO:1155.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;

XX haematopoiesis regulation; tissue growth; immunomodulator; activin;

XX inhibin; chemotaxis; chemokinesis; oncogenesis;

XX proliferation; metastasis; cancer; tumour; haematopoietic disorder;

XX myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

XX chronic inflammatory condition; proliferative retinopathy;

XX atherosclerosis; coronary heart disease; arterial ischaemia;

XX bone disorder; osteoporosis; vascular growth disorder;

XX tissue regeneration; wound healing; infection; immune disorder;

XX cell culture; drug screening; gene therapy; anti-inflammatory;

XX antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;

XX

KW cytosolic; osteopathic; vasotropic; cardiac; virocid; antibacterial;
 KW antifungal; vulnary; anticler; ss.
 XX Homo sapiens.
 XX WO200157188-A2.
 XX 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US003800.
 XX 03-FEB-2000; 2000US-00496914.
 XX 27-APR-2000; 2000US-00560875.
 XX (HYSE-) HYSEQ INC.
 XX Tang YF, Liu C, Drmanac RT;
 XX WPI: 2001-457740/49.
 XX P-PSDB; ABB12135.
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 PS Claim 1; Page 927; 1963pp; English.
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoietic regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a cDNA encoding a
 CC novel human polypeptide of the invention
 XX
 SQ Sequence 397 BP; 82 A; 114 C; 113 G; 88 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 397;
 Best Local Similarity 94.4%; Pred. No. 1.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CCGGAGGCGAGTGTGCG 18
 |||

DB 171 CCGGAGGCGAGTGTGCG 154
 RESULT 30
 ID ACH49668 standard; cDNA; 436 BP.
 AC ACH49668;
 XX 13-OCT-2003 (first entry)
 DT
 XX Human leukocyte cDNA #1262.
 DE
 XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KW genome mapping; biodiversity; genetic disorder.
 XX Homo sapiens.
 OS
 XX US2003073623-A1.
 XX 17-APR-2003.
 XX 30-JUN-2001; 2001US-00918995.
 XX 30-JUN-2001; 2001US-00918995.
 XX 30-JUN-2001; 2001US-00918995.
 XX (DRMA/) DRMANAC R T.
 XX (LABA/) LABAT I.
 XX (STAC/) STACHE-CRAIN B.
 XX (DICK/) DICKSON M C.
 XX (JONE/) JONES L W.
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI: 2003-615964/58.
 DR
 XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 PS Claim 1; SEQ ID NO 36880; 44pp; English.
 XX The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed Specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030073623
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 SQ Sequence 436 BP; 84 A; 148 C; 113 G; 91 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 8; Length 436;
 Best Local Similarity 94.4%; Pred. No. 1.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CCGGAGGCGAGTGTGCG 18
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90 CCGGAGGCGAGTGTGCG 73
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ABK42958/c
 ID ABK42958 standard; DNA; 942 BP.
 XX
 AC ABK42958;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Genomic sequence #857 encoding novel human connective tissue polypeptide.
 XX
 KW Human; connective tissue related disorder; cancer; gene therapy;
 KW Cystostatic; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200155343-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001322.
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 PR 31-JAN-2000; 2000US-0179065P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-565190/63.
XX
XX Nucleic acid encoding novel connective tissue associated polypeptides,
PT used in diagnosing, preventing, treating or ameliorating a disorder such
PT as cancer or rheumatoid arthritis.
XX
XX
XX Disclosure; SEQ ID NO 1845; 673pp; English.
XX
XX The present invention relates to the isolation of novel human connective
CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide
CC (cDNA and genomic) sequences encoding them. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with connective tissue(s), including
CC cancer. The polynucleotide sequences of the invention are also useful in
CC gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the
CC novel human connective tissue related polypeptides. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 942 BP; 200 A; 251 C; 240 G; 251 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 942;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 1; Indels 0; Gaps 0;

QY 1 CCCGGAGGCACTGTGC 18
Db 58 CCCGGAGGCACTGTGC 41

RESULT 32
ABK42959/C
ID ABK42959 standard; DNA; 942 BP.
XX
XX ABK42959;
AC
XX 21-MAY-2002 (first entry)
XX
XX
XX Genomic sequence #858 encoding novel human connective tissue polypeptide.
DE
XX
XX Human; connective tissue related disorder; cancer; gene therapy;
KW Cytostatic; gene; ds.
XX
XX Homo sapiens.
XX
XX WO200155343-A1.
PN
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XX 02-AUG-2001.
PD
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XX 17-JAN-2001; 2001WO-US001322.
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XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI, 2001-565190/63.	
XX		
XX		
PT	Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis.	
XX		
PS	Disclosure; SEQ ID NO 1846; 673pp; English.	
CC	The present invention relates to the isolation of novel human connective tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide (cDNA and genomic) sequences encoding them. The sequences of the	
CC		

Query Match	91.1%	Score 16.4	DB 4	Length 942
Best Local Similarity	94.4%	Pred. No. 1.7e+02		
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58	CCCGAGGCACTCTGTC	41		
RESULT 33				
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AC				
DT	04-DEC-2003 (first entry)			
DE	Connective tissue related genomic DNA #858.			
XX				
XX	cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;			
XX	antitumor; antileukemic; immunosuppressive; antihemagic; antiarthritis;			
XX	antiinflammatory; antiallergic; antiashmatic; dermatological;			
XX	nephrotic; virocidic; fungicide; antibacterial; antiparasitic;			
XX	gene therapy; ds; connective tissues disorder; rheumatoid arthritis;			
XX	systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;			
XX	Alzheimer's disease; neoplasia; leukaemia; neurodegenerative disorder;			
XX	Alzheimer's disease; Parkinson's disease; cardiovascular disease;			
XX	atherosclerosis; myocarditis; cardiopulmonary bypass complication;			
XX	autoimmune disease; multiple sclerosis; allergic reaction; asthma;			
XX	rheinitis; eczema; inflammatory condition; Crohn's disease; nephritis;			
XX	gastrointestinal disorder; inflammatory bowel disease;			
XX	organ transplant rejection; immune system disorder; Bruton's disease;			
XX	X-linked lymphoproliferative syndrome;			
XX	B-cell lymphoproliferative disorder; HIV; AIDS; infection;			
XX	chromosome identification; chromosome mapping;			
XX	connective tissue related polynucleotide; gene; ds.			
XX				
XX	Homo sapiens.			
XX				
XX	US2003054375-A1.			
XX				
XX	20-MAR-2003.			
XX				
XX	07-MAR-2002; 2002US-00092154.			
XX				
XX	31-JAN-2000; 2000US-0179065P.			
XX	04-FEB-2000; 2000US-0180628P.			
XX	24-FEB-2000; 2000US-0184664P.			
XX	02-MAR-2000; 2000US-0186350P.			
XX	16-MAR-2000; 2000US-0189874P.			
XX	17-MAR-2000; 2000US-0190076P.			
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XX	07-JUL-2000; 2000US-0216647P.			
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XX	26-JUL-2000; 2000US-0220563P.			

CC (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass
CC complications), autoimmune diseases (e.g. systemic lupus erythematosus,
rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.

Query Match 91.1%; Score 16.4; DB 8; Length 942;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTCTGCG 18
DB 58 CCCGAGGCGAGTCTGTC 41

RESULT 34

ID ADB6114/c
ADB6114 standard; DNA, 942 BP.

AC ADB6114;

DT 04-DEC-2003 (first entry)

XX Connective tissue related genomic DNA #857.

XX cytosolic; neuroprotective; noctropic; antiparkinsonian; cardiovascular;
XX antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic;
XX antiinflammatory; antiallergic; antiasthmatic; dermatological;
XX nephrotoxic; virucide; fungicide; antibacterial; antiparasitic;
XX gene therapy; ds; connective tissues disorder; rheumatoid arthritis;
XX systemic lupus erythematosus; scleroderma; Sjogrens syndrome; cancer;
XX cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;
XX Alzheimer's disease; Parkinson's disease; cardiovascular disease;
XX atherosclerosis; myocarditis; cardiopulmonary bypass complication;
XX autoimmune disease; multiple sclerosis; allergic reaction; asthma;
XX rinitis; eczema; inflammatory condition; Crohn's disease; nephritis;
XX gastrointestinal disorder; inflammatory bowel disease;
XX organ transplant rejection; immune system disorder; Britton's disease;
XX X-linked lymphoproliferative syndrome;
XX B-cell lymphoproliferative disorder; HIV; AIDS; infection;
XX chromosome identification; chromosome mapping;
XX connective tissue related polynucleotide; gene; ds.

OS Homo sapiens.

XX US2003054375-A1.

XX 20-MAR-2003.

PF 07-MAR-2002; 2002US-00092154.

XX 31-JAN-2000; 2000US-019065P.
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PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0231422P.
PR 08-SEP-2000; 2000US-0231433P.
PR 08-SEP-2000; 2000US-0231744P.
PR 08-SEP-2000; 2000US-0231813P.
PR 08-SEP-2000; 2000US-0231814P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231688P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 27-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.


```

XX DE p53 human tumour antigen antisense cDNA.
XX KW p53 human tumour antigen; antisense breast cancer therapy; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 4..138
XX FT /*tag= a
XX CA2090879-A.
XX PN
XX PD
XX PD 04-SEP-1994.
XX PF 03-MAR-1993; 93CA-02090879.
XX PR 03-MAR-1993; 93CA-02090879.
XX PA (PRED/) PREDDIE R E.
XX PI Freddie R E, Bergmann JE;
XX DR WPI: 1994-333671/42.
XX DR P-PSDB; AAR62645.
XX PT Novel reconstructed cDNA's and encoded proteins - are antisense to human
XX PT tumour antigen p53 gene, useful to provide breast cancer therapy.
XX PS Claim 1; Fig 1; 7pp; English.
XX CC AAQ72979 which encodes AAR62645 is the antisense strand to a p53 gene
XX CC human tumour antigen. In healthy women expression of AAR62645 is
XX CC repressed by the normal wild type p53 gene, however mutations in this
XX CC gene could permit the expression of this antisense protein, which may
XX CC lead to the development of breast cancer. Therefore AAR62645 can be used
XX CC in the development of humanised antibodies against breast cancer, which
XX CC due to AAR62645's non-expression in healthy women, should have no side
XX CC effects
XX SQ Sequence 140 BP; 30 A; 46 C; 44 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 88.9%; Score 16; DB 2; Length 140;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 3 CGAAGGCGAGTCTGGC 18
Db |||||
16 CGAAGGCGAGTCTGGC 31
XX
RESULT 37
AAQ74244
ID AAQ74244 standard; cDNA; 140 BP.
XX AC
XX AC AAQ74244;
XX DT 25-MAR-2003 (revised)
XX DT 02-JUN-1995 (first entry)
XX DE p53 antisense strand cDNA encoding protein BC538.
XX KW BC534; BC538; BC538.1; p53 antisense strand; breast cancer; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT misc_difference 7..9
XX FT /*tag= a
XX FT /transl_except= Ala
XX FT misc_difference 10..12
XX FT /*tag= b
XX FT /transl_except= Val

```

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FT FT misc_difference 13..15
FT FT /*tag= c
FT FT /transl_except= Thr
XX XX WO9421791-A1.
XX XX 29-SEP-1994.
XX PD
XX PD 04-MAR-1994; 94WO-EP000651.
XX PF 16-MAR-1993; 93US-00032843.
XX PR (BERG/) BERGMANN J E.
XX PA (PRED/) PREDDIE R E.
XX PI Bergmann JE, Freddie RE;
XX DR WPI: 1994-357732/44.
XX DR P-PSDB; AAR51626.
XX PT New p53 anti sense proteins - used to develop prods. for the diagnosis,
XX PT prediction and treatment of breast cancer and related cancers.
XX PS Claim 1; Fig 1C; 46pp; English.
XX XX
XX CC AAQ74243, AAQ74244 and AAQ74245 are cDNA fragments of the p53 gene
XX CC antisense strand which encode AAR51625 (BC534), AAR51626 (BC538) and
XX CC AAR51627 (BC538.1) respectively. These proteins can be used to develop
XX CC products which can be used in the diagnosis and prediction of breast
XX CC cancer and other cancers associated with mutations of the p53 gene.
XX CC These cancers can be treated by providing the patient with an inhibitor
XX CC of the BC534, BC538 and BC538.1 genes, and the regulatory sequence
XX CC AAQ74246 (BC53/reg). (Updated on 25-MAR-2003 to correct FN field.)
XX SQ Sequence 140 BP; 30 A; 46 C; 44 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 88.9%; Score 16; DB 2; Length 140;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 3 CGAAGGCGAGTCTGGC 18
Db |||||
16 CGAAGGCGAGTCTGGC 31
XX
RESULT 38
AAA70021
ID AAA70021 standard; cDNA; 184 BP.
XX AC
XX AC AAA70021;
XX DT 07-NOV-2000 (first entry)
XX DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO:332.
XX KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
XX KW tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
XX OS Homo sapiens.
XX XX WO200036107-A2.
XX PN
XX PD 22-JUN-2000.
XX PF 17-DEC-1999; 99WO-US030270.
XX PR 17-DEC-1999; 99US-00215681.
XX PR 17-DEC-1998; 98US-00216003.
XX PR 23-JUN-1999; 99US-00338933.
XX PR 24-SEP-1999; 99US-00404879.
XX PA (CORI-) CORIXA CORP.
XX

```

PI Mitcham JL, King GE, Algate PA, Frudakis TN;
DR WPI; 2000-431589/37.
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.
XX
XX
PS Claim 18; Page 180; 299pp; English.
CC The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC cancer. AA69691 to AA70077 and AB12552 to AB12557 represent human
CC ovarian carcinoma polynucleotides and proteins used in the
CC exemplification of the present invention
XX
SQ Sequence 184 BP; 61 A; 27 C; 47 G; 49 T; 0 U; 0 Other;
Query Match 85.6%; Score 15.4; DB 3; Length 184;
Best Local Similarity 94.1%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CCGGAGGCGCTGTGGC 18
DB 112 CCGAGAGGCGCTGTGGC 128
RESULT 39
ABN72915
ID ABN72915 standard; DNA; 184 BP.
XX
AC ABN72915;
XX
DT 02-JUL-2002 (first entry)
XX
DE Ovarian carcinoma antigen polynucleotide #20.
XX
KM Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
XX
OS Homo sapiens.
XX
PN WO200206317-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022635.
XX
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
XX
XX (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
XX WPI; 2002-164781/21.
XX
PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
XX Example 2; Page 298; 408pp; English.
CC This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion

CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents DNA related
CC to the invention
XX
SQ Sequence 184 BP; 61 A; 27 C; 47 G; 49 T; 0 U; 0 Other;
Query Match 85.6%; Score 15.4; DB 6; Length 184;
Best Local Similarity 94.1%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CCGGAGGCGCTGTGGC 18
DB 112 CCGAGAGGCGCTGTGGC 128
RESULT 40
ADA08485
ID ADA08485 standard; DNA; 184 BP.
XX
AC ADA08485;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human ovarian carcinoma antigen polynucleotide #330.
XX
KM ds; human; gene therapy; ovarian cancer; cancer.
XX
OS Homo sapiens.
XX
PN US2003091580-A1.
XX
PD 15-MAY-2003.
XX
PF 17-JUL-2001; 2001US-00907969.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
XX
XX Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
XX PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
XX WPI; 2003-532352/50.
XX
PT New isolated 0772P polypeptides and polynucleotides, useful in gene
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
PT cancer.
XX
XX Example 2; SEQ ID NO 332; 371pp; English.
XX
CC The invention relates to an isolated 0772P polypeptide, which has the
CC structure fully defined in the specification. The composition containing
CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
CC or antigen presenting cells are useful for stimulating an immune response
CC and treating ovarian cancer. Detecting the presence of the
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
CC carcinoma cDNAs and protein cDNAs were identified using microarray
CC technology. The present sequence represents a human ovarian carcinoma
CC antigen polynucleotide.
XX
SQ Sequence 184 BP; 61 A; 27 C; 47 G; 49 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 8; Length 184;
Best Local Similarity 94.1%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGGAGGCGAGTCTGGC 18
|||
Db 112 CCAGAGGCGAGTCTGGC 128

RESULT 41
AA129201/c
ID AA129201 standard; cDNA; 405 BP.

AC AA129201;

DT 12-OCT-2001 (first entry)

DE Colon tumour related determined cDNA sequence for clone R0093:H07.

XX Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;
KW gene therapy; vaccine; colonic cancer; ss.

XX Homo sapiens.

XX WC200149716-A2.

XX 12-JUL-2001.

XX 29-DEC-2000; 2000WC-US035596.

XX 30-DEC-1999; 99US-00476296.

XX 10-JAN-2000; 2000US-00480321.

XX 15-FEB-2000; 2000US-00504629.

XX 06-MAR-2000; 2000US-00519444.

XX 19-MAY-2000; 2000US-00575251.

XX 29-JUN-2000; 2000US-00609448.

XX 28-AUG-2000; 2000US-00649811.

XX (CORI-) CORIXA CORP.

XX Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;
PI King GE, Wang T, Jiang Y;
DR WPI; 2001-441847/47.

XX Colon tumor associated proteins and nucleic acids useful for the
PT prevention, diagnosis and treatment of colonic cancer.
XX Claim 2; Page 347; 472pp; English.

XX The present invention describes colon tumour associated proteins (I) and
CC the polynucleotides (II) that encode them. (I) have cytoskeletal activity.
CC (I) and (II) can be used in gene therapy and vaccine production. (I) and
CC (II) may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate colon tumour associated protein (TCAP)
CC expression, such as colonic cancer. For example, (I) and (II) may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC TCAPs by expressing inactive proteins or to supplement the patients own
CC production of them. Additionally, (II) may be used to produce the TCAP
CC proteins by inserting the nucleic acids into a host cell culturing the
CC cell to express the protein. (II) and its complementary sequences may
CC also be used as DNA probes in diagnostic polymerase chain reaction (PCR)
CC and hybridisation assays to detect and quantitate the presence of similar
CC nucleic acids in samples, and therefore which patients may be in need of
CC restorative therapy. (I) may also be used as antigens in the production
CC of antibodies against TCAPs and in assays to identify modulators of TCAP
CC expression and activity. Anti-(I) antibodies and antagonists may also be
CC used to down regulate TCAP expression and activity. The anti-(I)
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of TCAPs in samples (e.g. by enzyme linked immunosorbent assay
CC (ELISA)). AA128460 to AA129512 and AA244494 to AA24523 represent
CC nucleotide and amino acid sequences given in the exemplification of the

CC present invention

XX Sequence 405 BP; 106 A; 100 C; 77 G; 117 T; 0 U; 5 Other;

QY Query Match 85.6%; Score 15.4; DB 4; Length 405;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGGAGGCGAGTCTGGC 18
|||
Db 213 CCAGAGGCGAGTCTGGC 197

RESULT 42
AB233387/c
ID AB233387 standard; cDNA; 405 BP.

AC AB233387;

DT 30-JAN-2003 (first entry)

DE Human colon tumour cDNA for clone R0093:H07 SEQ ID NO:755.

XX Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer;
KW tumour; immune response; immunostimulant; cytostatic; vaccine; gene; ss.

XX Homo sapiens.

XX WC200283070-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002WC-US011475.

XX 10-APR-2001; 2001US-00833263.

XX 03-AUG-2001; 2001US-00922217.

XX 19-DEC-2001; 2001US-00025380.

XX (CORI-) CORIXA CORP.

XX Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;
PI Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD, Skelky YAW;
PI Fanger GR, Vedvick JS, Carter D;

XX WPI; 2003-067548/06.

XX New polynucleotide, useful for the preparation of a composition for
PT stimulating an immune response against, or treating, cancer.

XX Disclosure; Page 349; 537pp; English.

XX The present invention describes compounds (1) for the immunotherapy and
CC diagnosis of colon cancer. Also described: (1) a method for detecting the
CC presence of cancer in a patient; (2) a method for stimulating and/or
CC expanding T cells specific for a tumour protein; (3) an isolated T cell
CC population comprising T cells prepared by the method of (2); (4) a method
CC for stimulating an immune response in a patient; (5) a method for
CC treating cancer in a patient; and (6) a method for inhibiting the
CC development of cancer in a patient. (I) have immunostimulant and
CC cytostatic activities and can be used in vaccines. AB233646 to AB233725
CC and ABP55343 to ABP55391 represent human colon cancer/tumour related
CC sequences used in the exemplification of the present invention

XX Sequence 405 BP; 106 A; 100 C; 77 G; 117 T; 0 U; 5 Other;

QY Query Match 85.6%; Score 15.4; DB 7; Length 405;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGGAGGCGAGTCTGGC 18
|||
Db 213 CCAGAGGCGAGTCTGGC 197

RESULT 43
ACD95349/c
ID ACD95349 standard; cDNA; 428 BP.
XX
AC ACD95349;
XX
DT 23-SEP-2003 (first entry)
XX
DE Human colon cancer cell expressed cDNA #3761.
XX
KM Open reading frame detection; genome sequencing; colon cancer;
KM breast cancer; population genome analysis; genetic shift; cancer;
KM antibiotic resistance; antibiotic non-tolerance; congenital disease;
KM agriculture; food crop genome; resistance gene; retrovirus;
KM influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KM gene; ss.
XX
OS Homo sapiens.
XX
PN US2002155438-A1.
XX
PD 24-OCT-2002.
XX
PE 27-SEP-1999; 99US-00406117.
XX
PR 20-NOV-1998; 98US-00196716.
XX
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
XX
PI Simpson AJG, Neto ED, Brentani RR;
XX
DR WPI; 2003-182626/18.
XX
PT Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.
XX
PS Example 9; Page 548; 959pp; English.
XX
CC The invention describes a method of determining open reading frames in
CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (II), amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing, resulting
CC nucleic acids. The method is useful for determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a
CC nucleotide sequence of an open reading frame; for preparing a contig,
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. Further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as

CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library
XX

SO Sequence 428 BP; 123 A; 101 C; 79 G; 125 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 7; Length 428;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAGAGGAGCTGTGCG 18
DB 33 CAGGAGGAGCTGTGCG 17

RESULT 44
ID ABK39596/c
XX ABK39596 standard; cDNA; 447 BP.
XX
AC ABK39596;
XX
DT 21-MAY-2002 (first entry)
XX
DE cDNA encoding lung tumour protein clone R0129.G02.
XX
KM Lung tumour; cancer; T cell; immune response stimulator; cytostatic;
KM gene; ss.
XX
OS Homo sapiens.
XX
PN WO200204514-A2.
XX
PD 17-JAN-2002.
XX
PE 10-JUL-2001; 2001WO-US022058.
XX
PR 11-JUL-2000; 2000US-00614124.
XX
PR 29-AUG-2000; 2000US-00651563.
XX
PR 08-SEP-2000; 2000US-00658824.
XX
PR 26-SEP-2000; 2000US-00671325.
XX
PR 06-OCT-2000; 2000US-00677419.
XX
PR 30-OCT-2000; 2000US-00702705.
XX
PR 13-DEC-2000; 2000US-00736457.
XX
PR 03-MAY-2001; 2001US-00849626.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Matanabe Y, Henderson RA, Johnson JC, Retter MM;
PI Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS, Mcnabb A;
PI Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;
XX
DR WPI; 2002-164634/21.
XX
PT Novel polynucleotide encoding a lung tumor polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumor protein.
XX
PS Claim 1; SEQ ID NO 1634; 223pp; English.
XX
CC The invention describes an isolated polynucleotide and polypeptide useful
CC for stimulating and/or expanding T cells specific for a tumor protein
CC for determining the presence of a cancer in a patient. A composition
CC containing the polynucleotide and/or polypeptide is useful for treating a
CC lung cancer in a patient. The polypeptide is useful for removing tumor
CC cells from a biological sample. The polynucleotide is also useful as
CC probe or primer to detect the level of mRNA encoding a tumor protein.
CC This sequence encodes a lung tumour associated protein or protein
CC fragment, described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 447 BP; 129 A; 105 C; 80 G; 133 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 447;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGCG 18
DB 73 CCGAAGGCGAGTCTGCG 57

RESULT 45
ACAI1925/c
ID ACAI1925 standard; cDNA; 447 BP.
AC ACAI1925;
XX ACAI1925;
DT 05-JUN-2003 (first entry)
XX
DE Human lung adenocarcinoma library; cDNA SEQ ID 1634.
XX
KM Human; lung cancer; ss; lung tumour; cytostatic; vaccine;
KW T cell expansion; CD4; CD8.
XX
OS Homo sapiens.
XX
PN US2002197669-A1.
XX
PD 26-DEC-2002.
XX
PF 03-MAY-2001; 2001US-00849626.
XX
PR 13-DEC-2000; 2000US-00736457.
XX
PA (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (WANG/) WANG T.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
XX
PI Bangur CS, Fanger GR, Wang A, Wang T, Switzer AP, McNeill PD;
PI Clapper JD;
XX
DR WPI; 2003-352750/33.
XX
PT Novel lung cancer polynucleotide encoding lung cancer protein, useful for
PT detecting the presence of lung cancer in a patient, and in pharmaceutical
PT compositions, e.g. vaccines, for treating lung cancer.
XX
PS Example 1; Page; 72pp; English.

CC The invention relates to a polynucleotide encoding a lung tumour protein,
CC comprising a sequence selected from any of the 14 sequences mentioned in
CC the specification, or a sequence (S2) mentioned in specification,
CC complement of S1, sequences consisting of at least 20 contiguous residues
CC of S1, sequences that hybridise to S1, sequences having 75%, preferably
CC 90%, identity to S1, or degenerate variants of S1. Also included are an
CC isolated polypeptide (comprising a sequence (S3) selected from any one of
CC the 4 amino acid sequences mentioned in the specification, a sequence
CC encoded by the polynucleotide, or sequences having at least 70%,
CC preferably 90%, identity to a sequence encoded by the polynucleotide), an
CC expression vector comprising the polynucleotide operably linked to an
CC expression control sequence, a host cell transformed or transfected with
CC the vector, an isolated antibody (or its antigen-binding fragment) that
CC specifically binds to the polypeptide, detecting the presence of a cancer
CC in a patient, a fusion protein comprising the polypeptide, an
CC oligonucleotide that hybridises to S1 under moderately stringent
CC conditions, stimulating and/or expanding T cells specific for a tumour
CC protein (comprising contacting T cells with the polynucleotide, protein
CC or antigen-presenting cells, under conditions and for a time sufficient
CC to permit the stimulating and/or expansion of T cells) and inhibiting the
CC development of a cancer in a patient (by incubating CD4⁺ and/or CD8⁺ T
CC cells isolated from a patient with the polynucleotide, protein or antigen

CC presenting cells that express the polynucleotide, such that T cells
CC proliferate, administering to the patient an effective amount of the
CC proliferated T cells, and thus inhibiting the development of a cancer in
CC the patient. The polynucleotide, protein and cells are useful in a
CC composition for stimulating an immune response in a patient, and for
CC treating a cancer in a patient (particularly lung cancer). The
CC oligonucleotide is useful for determining the presence of a cancer in a
CC patient. The protein and oligonucleotides are useful in pharmaceutical
CC compositions, e.g. vaccines. The polynucleotide is also useful as a probe
CC or primer for nucleic acid hybridisation, and in the design and
CC preparation of ribozyme molecules for inhibiting expression of tumour
CC polypeptides and proteins in tumour cells. An amplified portion of the
CC polynucleotide is useful for isolating a full-length gene from a suitable
CC library. The present sequence is a cDNA (full length, extended or
CC partial) isolated from a library derived from lung tumour/cancer cells.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO at seqdata.uspto.gov/sequence.html?docId=20020197669

QY 2 CCGAAGGCGAGTCTGCG 18
DB 73 CCGAAGGCGAGTCTGCG 57

RESULT 46
ACAI0311/c
ID ACAI0311 standard; cDNA; 447 BP.
AC ACAI0311;
XX
DT 22-MAY-2003 (first entry)
XX
DE Lung cancer therapy and diagnosis associated cDNA #1600.
XX
KM Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002172952-A1.
XX
PD 21-NOV-2002.
XX
PF 10-JUL-2001; 2001US-00902941.
XX
PR 30-JUN-1999; 99US-00346492.
PR 15-OCT-1999; 99US-00419356.
PR 17-DEC-1999; 99US-00466867.
PR 30-DEC-1999; 99US-00476300.
PR 06-MAR-2000; 2000US-00518642.
PR 22-MAR-2000; 2000US-0053077.
PR 10-APR-2000; 2000US-00546259.
PR 27-APR-2000; 2000US-00560406.
PR 05-JUN-2000; 2000US-00589184.
PR 11-JUL-2000; 2000US-00614124.
PR 29-AUG-2000; 2000US-00651563.
PR 08-SEP-2000; 2000US-00658824.
PR 26-SEP-2000; 2000US-00671325.
PR 06-OCT-2000; 2000US-00677419.
PR 30-OCT-2000; 2000US-00702705.
PR 13-DEC-2000; 2000US-00736457.
PR 03-MAY-2001; 2001US-00849626.
XX
XX (CORI-) CORIXA CORP.
XX
PA Henderson RA, Wang T, Watanabe Y, Johnson JC, Retter MW,
PI Durham M, Carter D, Fanger GR, Vedvick TS, Bangur CS, McNabb A;

DR WPI; 2003-328427/31.
 XX
 PT New polynucleotide, useful for preparing a composition for treating or
 PT inhibiting development of cancer, e.g. lung cancer.
 XX
 PS Example 1; SEQ ID NO 1634; 82pp; English.
 XX
 CC The invention describes an isolated polynucleotide comprising one of 32
 CC sequences, complement or degenerate variants of them. The polynucleotide
 CC is useful for preparing a composition e.g. a vaccine or for gene therapy,
 CC for treating or inhibiting development of cancer, e.g. lung cancer. This
 CC sequence represents a polynucleotide associated with the compositions and
 CC methods for the therapy and diagnosis of lung cancer
 XX
 SQ Sequence 447 BP; 129 A; 105 C; 80 G; 133 T; 0 U; 0 Other;
 QY
 Query Match 85.6%; Score 15.4; DB 7; Length 447;
 Best Local Similarity 94.1%; Pred. No. 5.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 2 CCGAAGGCGACTCTGGC 18
 73 CCGAAGGCGACTCTGGC 57
 RESULT 47
 ACH26026/c
 ID ACH26026 standard; cDNA; 476 BP.
 XX
 AC ACH26026;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human adult ovary cDNA #4406.
 XX
 KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KW genome mapping; biodiversity; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2003073623-A1.
 PD 17-APR-2003.
 XX
 PF 30-JUL-2001; 2001US-00918995.
 XX
 PR 30-JUL-2001; 2001US-00918995.
 XX
 PA (DRNA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LM;
 PI WPI; 2003-615964/58.
 DR
 XX
 PT New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridisation probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX
 PS Claim 1; SEQ ID NO 13238; 44pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations

CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20030073623
 XX
 SQ Sequence 476 BP; 130 A; 116 C; 91 G; 135 T; 0 U; 4 Other;
 QY
 Query Match 85.6%; Score 15.4; DB 8; Length 476;
 Best Local Similarity 94.1%; Pred. No. 5.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 2 CCGAAGGCGACTCTGGC 18
 258 CCGAAGGCGACTCTGGC 242
 RESULT 48
 AAA16201/c
 ID AAA16201 standard; DNA; 633 BP.
 XX
 AC AAA16201;
 XX
 DT 14-JUN-2000 (first entry)
 XX
 DE Human colon cancer differentially expressed nucleotide sequence #206.
 XX
 KW Colon cancer; detect; differential expression; human; treatment;
 KW detect mutation; non-invasive diagnostic method; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200012702-A2.
 PD 09-MAR-2000.
 XX
 PF 30-AUG-1999; 99WO-US019424.
 XX
 PR 31-AUG-1998; 98US-0098639P.
 PR 27-JAN-1999; 99US-0117393P.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Endege WO, Steinmann KE, Aetle JH, Burgess CC, Carroll EJ;
 PI Catino TJ, Dwiwedi P, Ford DM, Lewis ME, Molino GA, Monahan JE;
 PI Schlegel R;
 PI WPI; 2000-256641/22.
 DR
 XX
 PT Novel nucleic acids and proteins for identifying therapeutic agents
 PT useful for treating and diagnosing cancer, especially colon cancer.
 XX
 PS Claim 16; Page 206; 345pp; English.
 XX
 CC This sequence represents a human nucleotide sequence which is
 CC differentially expressed in colon cancer cells compared to the expression
 CC levels in normal cells. The nucleotide sequence can be used as a source
 CC of primers and probes. The nucleotide sequence is useful for determining
 CC the phenotype of a cell by detecting the differential expression of the
 CC sequence relative to a normal cell. The probes derived from the sequence
 CC can also be used to determine the phenotype of cells in a sample. Probes
 CC and antibodies which hybridise to the nucleotide sequence can also be
 CC used to determine the phenotype of a cell. The primers are useful for
 CC detecting a mutation in a test nucleotide sequence and also for detecting
 CC cancer, preferably colon cancer. Antibodies against the protein encoded
 CC by the nucleotide sequence can also be used in a method to detect colon
 CC cancer. The diagnostic method is non-invasive and accurate for diagnosing
 CC colon cancer at an early stage
 XX

SQ Sequence 633 BP; 188 A; 151 C; 120 G; 172 T; 0 U; 2 Other;
Query Match 85.6%; Score 15.4; DB 3; Length 633;
Best Local Similarity 94.1%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCGAGAGGAGCTCTGGC 18
DB 426 CCAGAGGAGGAGCTCTGGC 410

RESULT 49
AAFI7596
ID AAFI7596 standard; cDNA; 647 BP.
XX
AC AAFI7596;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human breast cancer associated coding sequence #8.
XX
KW Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss.
XX
OS Homo sapiens.
XX
FN WO200060076-A2.
XX
PD 12-OCT-2000.
XX
PF 15-FEB-2000; 2000WO-US005308.
XX
PR 02-APR-1999; 99US-00285480.
PR 23-JUN-1999; 99US-00339338.
PR 02-SEP-1999; 99US-00389681.
PR 03-NOV-1999; 99US-00433826.
XX
PA (CORI-) CORIXA CORP.
XX
PI Yuqiu J, Dillon DC, Mitcham JL, Xu J, Harlocker SL;
XX
DR WPI; 2001-122627/13.
XX
XX
XX An isolated polypeptide useful for the treatment and diagnosis of tumors
PT e.g. breast cancer comprises at least an immunogenic portion of a breast
PT tumor protein.
XX
PS Claim 66; Page 110; 238pp; English.
XX
CC The present invention provides the coding sequences and some protein
CC sequences of proteins associated with breast cancer in humans. These
CC sequences can be used in the diagnosis and treatment of cancers,
CC particularly breast tumours
XX
SQ Sequence 647 BP; 216 A; 112 C; 129 G; 189 T; 0 U; 1 Other;
Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCGAGAGGAGCTCTGGC 18
DB 575 CCAGAGGAGGAGCTCTGGC 591

RESULT 50
AAS47026
ID AAS47026 standard; cDNA; 647 BP.
XX
AC AAS47026;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human breast cancer cDNA clone #8.

XX
KW Human; ss; breast cancer protein; tumour; cancer; cytostatic;
KW gene therapy.
XX
OS Homo sapiens.
XX
FN WO200179286-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US012164.
XX
PR 17-APR-2000; 2000US-00551621.
PR 08-JUN-2000; 2000US-00590751.
PR 22-JUN-2000; 2000US-00604287.
PR 20-JUL-2000; 2000US-00620405.
XX
PA (CORI-) CORIXA CORP.
XX
PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
XX
DR WPI; 2001-611721/70.
XX
XX
XX Breast Tumor Proteins and nucleic acids useful for the prevention,
PT diagnosis and treatment of breast cancer.
XX
PS Claim 37; Page 169; 297pp; English.
XX
XX
XX The invention relates to isolated breast tumour proteins and nucleic
CC acids that encode them, including immunogenic fragments of the proteins.
CC Also included are expression vectors expressing the proteins, transformed
CC cells and antibodies raised against the proteins or an antigen presenting
CC cell expressing the protein. The proteins and nucleic acids may be used
CC in the prevention, diagnosis and treatment of diseases associated with
CC inappropriate breast tumour protein expression, i.e. breast tumours and
CC breast cancer e.g. by gene therapy. The nucleic acids and their
CC complements may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC proteins, nucleic acids and antibodies may be used in assays to identify
CC modulators (e.g. antagonists) of breast tumour protein expression and
CC activity. The antibodies and antagonists may also be used to down
CC regulate expression and activity. The antibodies may also be used as
CC diagnostic agents for detecting the presence of the proteins in samples
CC (e.g. by enzyme linked immunosorbent assay (ELISA)) and in other immuno-
CC purification diagnostic techniques. The present sequence is a cDNA from a
CC breast tumour cDNA library isolated by subtractive hybridisation against
CC a normal breast cDNA library
XX
SQ Sequence 647 BP; 216 A; 112 C; 129 G; 189 T; 0 U; 1 Other;
Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCGAGAGGAGCTCTGGC 18
DB 575 CCAGAGGAGGAGCTCTGGC 591

Search completed: March 5, 2004, 00:08:07
Job time : 354 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 22:59:05 ; Search time 1556 Seconds

(without alignments)
501.398 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 cccggaagcagctctggc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 200 summaries

Database :
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_iny:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_man:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgc_hum:*
40: em_htgc_mus:*
41: em_htgc_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	AX298039	AX298039 Sequence
2	18	100.0	36	AX298040	AX298040 Sequence
3	18	100.0	102	I22245	I22245 Sequence 15
4	18	100.0	102	HMP5302	M13112 Homo sapien
5	18	100.0	133	AR060418	AR060418 Sequence
6	18	100.0	133	AR128976	AR128976 Sequence
7	18	100.0	133	I22232	I22232 Sequence 2
8	18	100.0	133	HMP53A02	M22882 Human phosp
9	18	100.0	140	A69972	A69972 Sequence 3
10	18	100.0	167	AF209128	AF209128 Homo sapi
11	18	100.0	167	AF209129	AF209129 Homo sapi
12	18	100.0	167	AF209130	AF209130 Homo sapi
13	18	100.0	167	AF209131	AF209131 Homo sapi
14	18	100.0	167	AF209132	AF209132 Homo sapi
15	18	100.0	167	AF209133	AF209133 Homo sapi
16	18	100.0	167	AF209134	AF209134 Homo sapi
17	18	100.0	167	AF209135	AF209135 Homo sapi
18	18	100.0	167	AF210336	AF210336 Homo sapi
19	18	100.0	167	AF210337	AF210337 Homo sapi
20	18	100.0	255	A40037	A40037 Sequence 5
21	18	100.0	255	A69974	A69974 Sequence 5
22	18	100.0	800	I92481	I92481 Sequence 1
23	18	100.0	1303	I22243	I22243 Sequence 13
24	18	100.0	1303	AX006172	AX006172 Sequence
25	18	100.0	1303	BD073938	BD073938 Assay, re
26	18	100.0	1303	HMTPE53B	M14695 Human p53 c
27	18	100.0	1307	I22242	I22242 Sequence 12
28	18	100.0	1307	HMTPE53A	M14694 Human p53 c
29	18	100.0	1317	A67149	A67149 Sequence 6
30	18	100.0	1317	AR064393	AR064393 Sequence
31	18	100.0	1317	AR123180	AR123180 Sequence
32	18	100.0	1317	AR157699	AR157699 Sequence
33	18	100.0	1317	I28707	I28707 Sequence 1
34	18	100.0	1317	I89361	I89361 Sequence 1
35	18	100.0	1317	AR181303	AR181303 Sequence
36	18	100.0	1317	AR218593	AR218593 Sequence
37	18	100.0	1317	AX057140	AX057140 Sequence
38	18	100.0	1317	AX203243	AX203243 Sequence
39	18	100.0	1317	BD064183	BD064183 Methods fo
40	18	100.0	1317	HSP53	X02465 Human mRNA
41	18	100.0	1760	E13558	E13558 Mutated p53
42	18	100.0	1760	E13737	E13737 cDNA encodi
43	18	100.0	1760	BD084820	BD084820 Diagnosis
44	18	100.0	1760	HMP53T	K03199 Human p53 c
45	18	100.0	2355	AF192534	AF192534 Expression
46	18	100.0	2451	AB082923	AB082923 Homo sapi
47	18	100.0	2508	BC003596	BC003596 Homo sapi
48	18	100.0	2521	AF307851	AF307851 Homo sapi
49	18	100.0	3407	HOMOTSPI	AF135120 Homo sapi
50	18	100.0	3423	HSW059JPI	X54156 Human p53 g
51	18	100.0	20303	HSP53G	U94758 Human p53 g
52	18	100.0	20303	HSU94788	AC087388 Homo sapi
53	18	100.0	121017	AC087388	AC087388 Homo sapi
54	18	100.0	163542	AC129071	AC129071 Pan trogl
55	18	100.0	166941	AC008049	AC008049 Homo sapi
56	18	100.0	218485	AC127470	AC127470 Pan trogl
57	18	100.0	28	I06689	I06689 Sequence 2
58	17	94.4	68749	AC118242	AC118242 Mus muscu
59	17	94.4	219468	AL592215	AL592215 Mouse DNA
60	17	94.4	219720	AC023364	AC023364 Mus muscu
61	17	94.4	316050	BCX21859	BCX21859 Xenopus 1
62	16.4	91.1	577	AR360397	AR360397 Xenopus 1
63	16.4	91.1	1986	AX202072	AX202072 Sequence
64	16.4	91.1	1846	MACP53A	L20442 Rhesus monk
65	16.4	91.1	59257	AC106019	AC106019 Homo sapi

Pred. No. is the number of results predicted by chance to have a

C 66	15.4	91.1	65545	2	AC139371	Homo sapi	C 139	15.4	85.6	11452	1	AE006030	Caulobact
C 67	15.4	91.1	70946	9	AL161614	Human DNA	C 140	15.4	85.6	13427	1	AE015175	AE015175 Shigella
C 68	15.4	91.1	121826	9	AL354935	Human DNA	C 141	15.4	85.6	13823	1	D90812	D90812 E.coli geno
C 69	15.4	91.1	158892	2	AC132819	Homo sapi	C 142	15.4	85.6	28798	9	HS001107	Y11107 Homo sapien
C 70	15.4	91.1	164282	2	AC015733	Homo sapi	C 143	15.4	85.6	34642	9	AC003965	AC003965 Homo sapi
C 71	15.4	91.1	166525	2	AC022413	Homo sapi	C 144	15.4	85.6	41721	9	AC145291	AC145291 Homo sapi
C 72	15.4	91.1	170212	9	AC058822	Homo sapi	C 145	15.4	85.6	49736	1	AF319988	AF319988 Stigmarel
C 73	15.4	91.1	174521	2	AC127468	Papio anu	C 146	15.4	85.6	52603	9	AC016585	AC016585 Homo sapi
C 74	15.4	91.1	176927	2	AC127469	Papio anu	C 147	15.4	85.6	60966	9	AC003030	AC003030 Homo sapi
C 75	15.4	91.1	196037	9	AC129492	Homo sapi	C 148	15.4	85.6	63544	2	AC145792	AC145792 Silurana
C 76	15.4	91.1	196838	2	AC151596	Rattus no	C 149	15.4	85.6	67016	9	AC008767	AC008767 Homo sapi
C 77	15.4	91.1	196840	2	AC023255	Rattus no	C 150	15.4	85.6	76655	4	AC091723	AC091723 Sus scrof
C 78	15.4	91.1	231746	2	AC013889	Homo sapi	C 151	15.4	85.6	77489	2	AC139552	AC139552 Homo sapi
C 79	15.4	91.1	231109	2	AC011864	Mus muscu	C 152	15.4	85.6	78419	3	AC004639	AC004639 Homo sapi
C 80	15.4	91.1	233908	2	AC112290	Rattus no	C 153	15.4	85.6	81786	9	AC003002	AC003002 Homo sapi
C 81	15.4	91.1	233678	2	AC110557	Rattus no	C 154	15.4	85.6	82019	2	AC139567	AC139567 Homo sapi
C 82	15.4	91.1	257092	2	AC097308	Rattus no	C 155	15.4	85.6	89885	3	AC004368	AC004368 Drosophill
C 83	15.4	91.1	282895	2	AC096056	Rattus no	C 156	15.4	85.6	91099	9	AC110280	AC110280 Homo sapi
C 84	15.4	88.9	140	6	AA0035	Sequence 3	C 157	15.4	85.6	93634	2	AC127088	AC127088 Homo sapi
C 85	15.4	88.9	144885	10	AL7731766	Mouse DNA	C 158	15.4	85.6	105692	2	AP003953	AP003953 Oryza sat
C 86	15.4	88.9	187081	10	AL7731766	Mouse DNA	C 159	15.4	85.6	110000	9	HS063451	HS063451 Continuation (2 of
C 87	15.4	88.9	214284	9	AC116643	Homo sapi	C 160	15.4	85.6	111293	9	AC000377	AC000377 Homo sapi
C 88	15.4	88.9	227769	2	AC112437	Rattus no	C 161	15.4	85.6	116215	9	AC004130	AC004130 Homo sapi
C 89	15.4	88.9	246913	2	AC113620	Rattus no	C 162	15.4	85.6	118873	9	HS118494	HS118494 Homo DNA
C 90	15.4	88.9	254175	2	AC096015	Rattus no	C 163	15.4	85.6	120831	4	AC137644	AC137644 Artibeus
C 91	15.4	88.9	254175	2	AC096015	Rattus no	C 164	15.4	85.6	122948	9	HS091821	HS091821 Homo sapi
C 92	15.4	88.9	254175	2	AC096015	Rattus no	C 165	15.4	85.6	127361	9	AC007283	AC007283 Homo sapi
C 93	15.4	88.9	254175	2	AC096015	Rattus no	C 166	15.4	85.6	131710	2	AC147500	AC147500 Mus muscu
C 94	15.4	88.9	254175	2	AC096015	Rattus no	C 167	15.4	85.6	132960	9	AC002403	AC002403 Homo sapi
C 95	15.4	88.9	254175	2	AC096015	Rattus no	C 168	15.4	85.6	132963	2	AC017518	AC017518 Drosophill
C 96	15.4	88.9	254175	2	AC096015	Rattus no	C 169	15.4	85.6	133815	9	AC124055	AC124055 Homo sapi
C 97	15.4	88.9	254175	2	AC096015	Rattus no	C 170	15.4	85.6	137271	2	AC102823	AC102823 Mus muscu
C 98	15.4	88.9	254175	2	AC096015	Rattus no	C 171	15.4	85.6	138347	9	AL389889	AL389889 Human DNA
C 99	15.4	88.9	254175	2	AC096015	Rattus no	C 172	15.4	85.6	144741	8	AP004674	AP004674 Oryza sat
C 100	15.4	88.9	254175	2	AC096015	Rattus no	C 173	15.4	85.6	148055	9	AC026414	AC026414 Homo sapi
C 101	15.4	88.9	254175	2	AC096015	Rattus no	C 174	15.4	85.6	148356	2	AC144886	AC144886 Bos tauru
C 102	15.4	88.9	254175	2	AC096015	Rattus no	C 175	15.4	85.6	153937	2	AC023953	AC023953 Homo sapi
C 103	15.4	88.9	254175	2	AC096015	Rattus no	C 176	15.4	85.6	156135	9	AC093799	AC093799 Homo sapi
C 104	15.4	88.9	254175	2	AC096015	Rattus no	C 177	15.4	85.6	156683	9	AC091891	AC091891 Homo sapi
C 105	15.4	88.9	254175	2	AC096015	Rattus no	C 178	15.4	85.6	157259	2	AC016976	AC016976 Homo sapi
C 106	15.4	88.9	254175	2	AC096015	Rattus no	C 179	15.4	85.6	158043	9	AC105270	AC105270 Homo sapi
C 107	15.4	88.9	254175	2	AC096015	Rattus no	C 180	15.4	85.6	158310	9	AL162571	AL162571 Human DNA
C 108	15.4	88.9	254175	2	AC096015	Rattus no	C 181	15.4	85.6	159056	10	AL0645368	AL0645368 Mouse DNA
C 109	15.4	88.9	254175	2	AC096015	Rattus no	C 182	15.4	85.6	162686	8	AT0506156	AT0506156 Amborella
C 110	15.4	88.9	254175	2	AC096015	Rattus no	C 183	15.4	85.6	163417	9	AC0050433	AC0050433 Homo sapi
C 111	15.4	88.9	254175	2	AC096015	Rattus no	C 184	15.4	85.6	163954	2	AC017185	AC017185 Drosophill
C 112	15.4	88.9	254175	2	AC096015	Rattus no	C 185	15.4	85.6	165857	9	AP006463	AP006463 Homo sapi
C 113	15.4	88.9	254175	2	AC096015	Rattus no	C 186	15.4	85.6	167254	2	AC146109	AC146109 Pan trogl
C 114	15.4	88.9	254175	2	AC096015	Rattus no	C 187	15.4	85.6	168652	9	AC022024	AC022024 Homo sapi
C 115	15.4	88.9	254175	2	AC096015	Rattus no	C 188	15.4	85.6	169873	2	AC079881	AC079881 Homo sapi
C 116	15.4	88.9	254175	2	AC096015	Rattus no	C 189	15.4	85.6	170595	2	AC025957	AC025957 Homo sapi
C 117	15.4	88.9	254175	2	AC096015	Rattus no	C 190	15.4	85.6	172574	2	AC011121	AC011121 Homo sapi
C 118	15.4	88.9	254175	2	AC096015	Rattus no	C 191	15.4	85.6	173055	2	AC118579	AC118579 Didelphis
C 119	15.4	88.9	254175	2	AC096015	Rattus no	C 192	15.4	85.6	173081	3	AC110170	AC110170 Mus muscu
C 120	15.4	88.9	254175	2	AC096015	Rattus no	C 193	15.4	85.6	173723	10	AC009351	AC009351 Drosophill
C 121	15.4	88.9	254175	2	AC096015	Rattus no	C 194	15.4	85.6	173846	10	AL2928065	AL2928065 Mouse DNA
C 122	15.4	88.9	254175	2	AC096015	Rattus no	C 195	15.4	85.6	173932	2	AC102837	AC102837 Mus muscu
C 123	15.4	88.9	254175	2	AC096015	Rattus no	C 196	15.4	85.6	175610	9	AC073176	AC073176 Homo sapi
C 124	15.4	88.9	254175	2	AC096015	Rattus no	C 197	15.4	85.6	175909	9	AC093559	AC093559 Homo sapi
C 125	15.4	88.9	254175	2	AC096015	Rattus no	C 198	15.4	85.6	178515	9	AC015551	AC015551 Homo sapi
C 126	15.4	88.9	254175	2	AC096015	Rattus no	C 199	15.4	85.6	179216	2	AC074016	AC074016 Homo sapi
C 127	15.4	88.9	254175	2	AC096015	Rattus no	C 200	15.4	85.6	179848	2	AC139880	AC139880 Lemur cat
C 128	15.4	88.9	254175	2	AC096015	Rattus no							
C 129	15.4	88.9	254175	2	AC096015	Rattus no							
C 130	15.4	88.9	254175	2	AC096015	Rattus no							
C 131	15.4	88.9	254175	2	AC096015	Rattus no							
C 132	15.4	88.9	254175	2	AC096015	Rattus no							
C 133	15.4	88.9	254175	2	AC096015	Rattus no							
C 134	15.4	88.9	254175	2	AC096015	Rattus no							
C 135	15.4	88.9	254175	2	AC096015	Rattus no							
C 136	15.4	88.9	254175	2	AC096015	Rattus no							
C 137	15.4	88.9	254175	2	AC096015	Rattus no							
C 138	15.4	88.9	254175	2	AC096015	Rattus no							

ALIGNMENTS

RESULT 1
DEFINITION Sequence 35 from Patent WO0183740.
LOCUS AX298039
ACCESSION AX298039
VERSION AX298039.1 GI:17128125

18 bp DNA
linear PAT 26-NOV-2001

KEYWORDS	SYNTHETIC CONSTRUCT
SOURCE	Synthetic construct
ORGANISM	Synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1 Iversen, P.L. and Hudziak, R.
TITLE	Splice-region antisense composition and method
JOURNAL	Patent: WO 0183740-A 35 08-NOV-2001;
FEATURES	Avi Biopharma, Inc. (US)
SOURCE	Location/Qualifiers
ORIGIN	1. 18
Query Match	/organism="synthetic construct"
Best Local Similarity	/mol_type="unassigned DNA"
Matches	/db_xref="taxon:33630"
	/note="antisense"
100.0%; Score 18; DB 6; Length 18;	
100.0%; Pred. No. 1.3e+03;	
0; Mismatches 0; Indels 0; Gaps 0;	
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1 CCCGGAAGGCGAGCTGGC 18	
AX298040	36 bp DNA linear PAT 26-NOV-2001
Sequence 36 from Patent WO0183740.	
AX298040	
AX298040.1 GI:17128126	
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1 Iversen, P.L. and Hudziak, R.
TITLE	Splice-region antisense composition and method
JOURNAL	Patent: WO 0183740-A 36 08-NOV-2001;
FEATURES	Avi Biopharma, Inc. (US)
SOURCE	Location/Qualifiers
ORIGIN	1. 36
Query Match	/organism="synthetic construct"
Best Local Similarity	/mol_type="unassigned DNA"
Matches	/db_xref="taxon:33630"
100.0%; Score 18; DB 6; Length 36;	
100.0%; Pred. No. 1e+03;	
0; Mismatches 0; Indels 0; Gaps 0;	
1 CCCGGAAGGCGAGCTGGC 18	
17 CCCGGAAGGCGAGCTGGC 34	
122245	102 bp DNA linear PAT 07-OCT-1996
Sequence 15 from patent US 5527676.	
122245	
122245.1 GI:1602599	
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 102)
AUTHORS	Vegetstein, B., Baker, S.J., Fearon, E.R. and Nigro, J.M.
TITLE	Detection of loss of the wild-type p53 gene and kine therefor
JOURNAL	Patent: US 5527676-A 15 18-JUN-1996;
FEATURES	Location/Qualifiers

	source	1..102	/organism="unknown"	
ORIGIN		/mol_type="unassigned DNA"		
Query Match		100.0%; Score 18; DB 6; Length 102;		
Best Local Similarity		100.0%; Pred. No. 7.8e+02;		
Matches	18; Conservative	0; Mismatches	0; Indels	0; Gaps
CY	1 CCCGAGGCACTGTGGC 18			
Db	20 CCCGAGGCACTGTGGC 3			
RESULT 4	HMP9302	102 bp	DNA	PRI 14-DEC-2000
LOCUS	HMP9302			
DEFINITION	Homo sapiens phosphoprotein p53 (TP53) gene, exon 2.			
ACCESSION	M13112			
VERSION	M13112.1 GI:189451			
KEYWORDS	antigen; phosphoprotein; tumor antigen.			
SEGMENT	2 of 11			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 102) Lamb,P. and Crawford,L. Characterization of the human p53 gene Mol. Cell. Biol. 6 (5), 1379-1385 (1986) 87064416			
JOURNAL				
MEDLINE				
PUBMED	2946935			
FEATURES				
source	location/Qualifiers			
	1..102			
	/organism="Homo sapiens"			
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	/map="17p13.1"			
exon	1..102			
	/gene="TP53"			
	/note="G00-120-445"			
	/number=2			
ORIGIN				
Query Match		100.0%; Score 18; DB 5; Length 102;		
Best Local Similarity		100.0%; Pred. No. 7.8e+02;		
Matches	18; Conservative	0; Mismatches	0; Indels	0; Gaps
CY	1 CCCGAGGCACTGTGGC 18			
Db	20 CCCGAGGCACTGTGGC 3			
RESULT 5	AR060418	133 bp	DNA	PAT 29-SEP-1999
LOCUS	AR060418/c			
DEFINITION	Sequence 22 from patent US 5840579.			
ACCESSION	AR060418			
VERSION	AR060418.1 GI:5986868			
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 133)			
AUTHORS	Boeke,U.D. and Brachmann,R.K.			
TITLE	Nucleic acids encoding p53 mutations which suppress p53 cancer mutations			
JOURNAL	Patent: US 5840579-A 22 24-NOV-1998;			
FEATURES	Location/Qualifiers			
source	1..133			
	/organism="unknown"			
	/mol_type="unassigned DNA"			

Query Match 100.0%; Score 18; DB 6; Length 133;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGGAGCTGTGGC 18
DB 35 CCCGAGGAGGAGCTGTGGC 18

RESULT 6
LOCUS AR128976/c 133 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6183964.
ACCESSION AR128976
VERSION AR128976.1 GI:14116638
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 133)
AUTHORS Boeke, U.D. and Brachmann, R.K.
TITLE Method for identifying suppressor mutations for common p53 cancer mutations
JOURNAL Patent: US 6183964-A 22 06-FEB-2001;
FEATURES
source location/Qualifiers
1.133
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 133;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGGAGCTGTGGC 18
DB 35 CCCGAGGAGGAGCTGTGGC 18

RESULT 7
LOCUS 122232/c 133 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 2 from patent US 5527676.
ACCESSION 122232
VERSION 122232.1 GI:1602586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 133)
AUTHORS Vogelstein, B., Baker, S.J., Fearon, E.R. and Nigro, J.M.
TITLE Detection of loss of the wild-type p53 gene and kits therefor
JOURNAL Patent: US 5527676-A 2 18-JUN-1996;
FEATURES
source location/Qualifiers
1.133
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 133;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGGAGCTGTGGC 18
DB 35 CCCGAGGAGGAGCTGTGGC 18

RESULT 8
LOCUS HUMF53A02/c 133 bp DNA linear PRI 08-JAN-1995
DEFINITION Human phosphoprotein p53 gene, exon 2.

ACCESSION M22882
VERSION M22882.1 GI:189465
KEYWORDS phosphoprotein p53.
SEGMENT 2 of 11
SOURCE Homo sapiens (human)

REFERENCE 1 (bases 1 to 133)
AUTHORS Buchman, V.L., Chumakov, P.M., Ninkina, N.N., Samarina, O.P. and Georgiev, G.P.
TITLE A variation in the structure of the protein-coding region of the human p53 gene
JOURNAL Gene 70 (2), 245-252 (1988)
MEDLINE 89108008
PubMed 2905688

COMMENT Original source text: Homo sapiens placenta DNA.
FEATURES
source location/Qualifiers
1.133
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="placenta"
order(M22881.1:397..412,<1..15)
/gene="p53"
/number=1
16.117
/gene="p53"
/product="phosphoprotein p53"
/number=2

ORIGIN

About 10400 bp after segment 1.
Query Match 100.0%; Score 18; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGGAGCTGTGGC 18
DB 35 CCCGAGGAGGAGCTGTGGC 18

RESULT 9
LOCUS A69972 140 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 3 from Patent WO9807851.
ACCESSION A69972
VERSION A69972.1 GI:4774443
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 140)
AUTHORS Predde, E.R. and Bergmann, J.E.
TITLE AGENTS FOR THE PRE-SYMPTOMATIC DETECTION, PREVENTION AND TREATMENT OF BRCA1 CANCER IN HUMANS
JOURNAL Patent: WO 9807851-A 3 26-FEB-1998;
FEATURES
source location/Qualifiers
1.140
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/db_xref="taxon:9606"
/clone="SC532L"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 140;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGGAGCTGTGGC 18
DB 14 CCCGAGGAGGAGCTGTGGC 31

RESULT 10
AF209128/c
LOCUS AF209128 167 bp DNA linear PRI 27-MAR-2003
DEFINITION Homo sapiens tumor suppressor p53 (TP53) gene, partial cds.
ACCESSION AF209128
VERSION AF209128.1 GI:7107284
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Thompson-Hehir,J., Davies,M.P., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
JOURNAL Novel polymerase chain reaction approach for full-coding p53 mutation detection in microdissected archival tumors
MEDLINE Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
PUBMED 20306720
REFERENCE
AUTHORS Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories, Clatterbridge Cancer Research Trust, Clatterbridge Hospital, Bebington, Wirral CH63 4UY, United Kingdom
LOCATION/Qualifiers
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1. .167
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/chromosome="17"
/tissue_type="ovarian carcinomas and associated normal tissues"
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intron
1. .21
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number=1
exon
22. .123
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number=2
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/db_xref="GI:7107285"
/translation="MEBPQSDPSVPEPLSGETPSDLMLK"
intron
124. .>167
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variation
150. .152
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/replace="cc"
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Query Match 100.0%; Score 18; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGGAAGGCACTCTGAC 18
DB 41 CCCGGAAGGCACTCTGAC 24
RESULT 11
AF209129/c
LOCUS AF209129 167 bp DNA linear PRI 27-MAR-2003

DEFINITION Homo sapiens tumor suppressor p53 (TP53) gene, partial cds.
ACCESSION AF209129
VERSION AF209129.1 GI:7107286
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Thompson-Hehir,J., Davies,M.P., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
JOURNAL Novel polymerase chain reaction approach for full-coding p53 mutation detection in microdissected archival tumors
MEDLINE Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
PUBMED 20306720
REFERENCE
AUTHORS Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories, Clatterbridge Cancer Research Trust, Clatterbridge Hospital, Bebington, Wirral CH63 4UY, United Kingdom
LOCATION/Qualifiers
source
1. .167
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/chromosome="17"
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intron
1. .21
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exon
22. .123
/gene="TP53"
number=2
50. .>123
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/protein_id="AAF36355.1"
/db_xref="GI:7107287"
/translation="MEBPQSDPSVPEPLSGETPSDLMLK"
intron
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number=2
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Query Match 100.0%; Score 18; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGGAAGGCACTCTGAC 18
DB 41 CCCGGAAGGCACTCTGAC 24
RESULT 12
AF209130/c
LOCUS AF209130 167 bp DNA linear PRI 27-MAR-2003
DEFINITION Homo sapiens tumor suppressor p53 (TP53) gene, partial cds.
ACCESSION AF209130
VERSION AF209130.1 GI:7107288
KEYWORDS
SOURCE Homo sapiens (human)

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ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE        1 (baes 1 to 167)
JOURNAL      Thompson-Hehir,J., Davies,M.P., Green,J.A., Halliwell,N.,
MEDLINE      Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
PUBMED       Novel polymerase chain reaction approach for full-coding p53
REFERENCE     mutation detection in microdissected archival tumors
AUTHORS      Diaon, Mol. Pathol. 9 (2), 110-119 (2000)
TITLE        20366720
JOURNAL      (baes 1 to 167)
PUBMED       10850547
REFERENCE     Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N.,
AUTHORS      Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE        Direct Submision
JOURNAL      Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories,
PUBMED       Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
REFERENCE     Beblington, Wirral CH63 4UY, United Kingdom
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            /number=2
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Best Local Similarity 100.0%; Pred. No. 6; 8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY              1 CCCGAAGGCGAGCTGGC 18
                |||||||
Db              41 CCCGAAGGCGAGCTGGC 24
RESULT 13
LOCUS      AF209131/c
DEFINITION Homo sapiens tumor suppressor p53 (TP53) gene, partial cds.
ACCESSION  AF209131
VERSION     AF209131.1 GI:7107290
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
AUTHORS     Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (baes 1 to 167)
JOURNAL     Thompson-Hehir,J., Davies,M.P., Green,J.A., Halliwell,N.,
PUBMED      Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE       Direct Submision
JOURNAL     Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories,
PUBMED      Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
REFERENCE     Beblington, Wirral CH63 4UY, United Kingdom

```

TITLE	Novel polymerase chain reaction approach for full-coding p53
JOURNAL	Diagn. Mol. Pathol. 9 (2), 110-115 (2000)
MEDLINE	20306720
REFERENCE	2 (bases 1 to 167)
AUTHORS	Thompson-Henit,J., Davies,M.P.A., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE	Direct Submission
JOURNAL	Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories, Clatterbridge Cancer Research Trust, Clatterbridge Hospital, Bebington, Wirral CH63 4UY, United Kingdom
FEATURES	Location/Qualifiers
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gene	<1..>167
	/gene="TP53"
intron	<1..21
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exon	/number=1
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	22..123
	/gene="TP53"
	/number=2
CDS	50..>123
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Best Local Similarity	100.0%; Pred. No. 6,8e+02;
Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
CY	1 CCGGAGGAGCAGCTGGC 18
Db	41 CCGGAGGAGCAGCTGGC 24
RESULT 14	
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LOCUS	Homo sapiens cell-line Molt4 tumor suppressor p53 (TP53) gene,
DEFINITION	partial cds.
ACCESSION	AF209132
VERSION	AF209132.1 GI:7107292
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Bakayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 167)
	Thompson-Henit,J., Davies,M.P., Green,J.A., Halliwell,N.,
TITLE	Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
	Novel polymerase chain reaction approach for full-coding p53
JOURNAL	mutation detection in microdissected archival tumors
MEDLINE	Diagn. Mol. Pathol. 9 (2), 110-115 (2000)

PUBMED 10850547
REFERENCE 2 (bases 1 to 167)
AUTHORS Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N.,
Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories,
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bedlington, Mirral CH63 4UY, United Kingdom
LOCATION/Qualifiers

FEATURES
source 1.167
/organism="Homo sapiens"
/mol_type="genomic DNA"
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CDS 50..>123
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QY 1 CCCGGAAGCAGCTGGC 18
Db 41 CCCGGAAGCAGCTGGC 24

RESULT 15
AF209133/c 167 bp DNA linear PRI 27-MAR-2003
LOCUS Homo sapiens cell-line A431 tumor suppressor p53 (TP53) gene,
DEFINITION partial cds.
ACCESSION AF209133
VERSION AF209133.1 GI:7107294
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 167)
TITLE Thompson-Hehir,J., Davies,M.P., Green,J.A., Halliwell,N.,
Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
REFERENCE Novel polymerase chain reaction approach for full-coding p53
mutation detection in microdissected archival tumors
JOURNAL Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
MEDLINE 20306720
PUBMED 10850547
REFERENCE 2 (bases 1 to 167)
AUTHORS Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N.,
Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories,
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bedlington, Mirral CH63 4UY, United Kingdom
LOCATION/Qualifiers

JOURNAL Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories,
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bedlington, Mirral CH63 4UY, United Kingdom
LOCATION/Qualifiers

FEATURES
source 1.167
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/gene="TP53"
/number=2
CDS 50..>123
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intron 124..>167
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/number=2
variation 150..152
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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
Db 41 CCCGGAAGCAGCTGGC 24

RESULT 16
AF209134/c 167 bp DNA linear PRI 27-MAR-2003
LOCUS Homo sapiens cell-line HT29 tumor suppressor p53 (TP53) gene,
DEFINITION partial cds.
ACCESSION AF209134
VERSION AF209134.1 GI:7107296
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 167)
TITLE Thompson-Hehir,J., Davies,M.P., Green,J.A., Halliwell,N.,
Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
REFERENCE Novel polymerase chain reaction approach for full-coding p53
mutation detection in microdissected archival tumors
JOURNAL Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
MEDLINE 20306720
PUBMED 10850547
REFERENCE 2 (bases 1 to 167)
AUTHORS Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N.,
Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories,
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bedlington, Mirral CH63 4UY, United Kingdom
LOCATION/Qualifiers

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Best Local Similarity	100.0%;	Pred. No. 6.8e+02;		
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	Dd	41 CCCGGAAGGCAGTCTGGC	24

RESULT 17	AF209135	167 bp	DNA	linear	PR1 27-MAR-2003
LOCUS	AF209135/c				
DEFINITION	AF209135	Homo sapiens cell-line HeLa tumor suppressor p53 (TP53) gene,			
ACCESSION	AF209135	partial cds.			
VERSION	AF209135.1	GI:7107298			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (pages 1 to 167)	Thompson-Hehir, J., Davies, M. P., Green, J. A., Halliwell, N., Joyce, K. A., Salisbury, J., Sisson, D. R., Vergote, I. and Walker, C.	Novel polymerase chain reaction approach for full-coding p53 mutation detection in microdissected archival tumors	Diagn. Mol. Pathol. 9 (2), 110-119 (2000)

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Beddington, Watlington OX63 4UY, United Kingdom

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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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124..>167
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2Y 1 CCCGGAAGGCAGTCTGGC 18
|||
41 CCCGGAAGGCAGTCTGGC 24
Db

RESULT 18	AF209136	167 bp	DNA	linear	PBT 27-MAR-2003
LOCUS	AF209136/c				
DEFINITION	Homo sapiens cell-line HNS tumor suppressor p53 (TP53) gene, partial cds.				
ACCESSION	AF209136				
VERSION	AF209136.1	GI:7107300			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 167)
Thompson,Hehir,J., Davies,M.P., Green,J.A., Halliwell,N.,
Joyce,K.A., Salisbury,J., Sissons,D.R., Vergote,I. and Walker,C
Novel polymerase chain reaction approach for full-coding p53
mutation detection in microdissected archival tumors
Diagn. Mol. Pathol. 9 (2), 110-119 (2000)

REFERENCE
2 (bass 1 to 167)
Thompson-Héhr, J., Davies, M.P.A., Green, U.A., Halliwell, N.,
Joyce, K.A., Salisbury, J., Sibson, D.R., Vergote, I. and Walker, C.
Direct Submission
Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bebington, Wirral CH63 4UJ, United Kingdom

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FEATURES
SOURCE
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/gene="TP53"
<1..21
intron
/gene="TP53"

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22..123
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/translation="MEEPQSPSYEPPLSQETFSIDLK"
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150..152
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intron

variation

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGAGGAGCAGTCTGCG 18
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41 CCCGAGGAGCAGTCTGCG 24

RESULT 19
AF210308S1 167 bp DNA linear PRI 12-APR-2000
LOCUS Homo sapiens p53 tumor suppressor protein (TP53) gene, exon 2.
DEFINITION AF210308
VERSION AF210308.1 GI:7542419
KEYWORDS
SEGMENT
1 of 3
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 167)
Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
Mutation Detection Utilizing a Novel PCR Approach for Amplification
of the p53 Gene from Microdissected Tissue: Application to Archival
Tumor Samples
Unpublished
2 (bases 1 to 167)
Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N.,
Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
Direct Submission
Submitted (01-DEC-1999) J.K. Douglas Cancer Research Laboratories,
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bedlington, Wirral CH63 4UY, UK
Location/Qualifiers
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misc_difference 152
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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
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41 CCCGAGGAGCAGTCTGCG 24

RESULT 20
A40037 255 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 5 from Patent WO9421791.
DEFINITION A40037
ACCESSION A40037
VERSION A40037.1 GI:2296203
KEYWORDS
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 255)
Bergman,J.E. and Predlie,R.E.
AGENTS FOR THE PREVENTION AND TREATMENT OF BREAST CANCER
Patent: WO 9421791-A 5 29-SEP-1994;
BERGMANN JOHANNA EUGENIE (DE)
Location/Qualifiers
1..255
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGAGGAGCAGTCTGCG 18
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14 CCCGAGGAGCAGTCTGCG 31

RESULT 21
A69974 255 bp DNA linear PAT 07-MAY-1999
LOCUS Sequence 5 from Patent WO9807851.
DEFINITION A69974
ACCESSION A69974
VERSION A69974.1 GI:4774444
KEYWORDS
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 255)
Predlie,R.R. and Bergmann,J.E.
AGENTS FOR THE PRE-SYMPTOMATIC DETECTION, PREVENTION AND TREATMENT
OF BREAST CANCER IN HUMANS
Patent: WO 9807851-A 5 26-FEB-1998;
PREDDIE ENRIQUE R (CA)
Location/Qualifiers
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/mol_type="unassigned DNA"
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGAGGAGCAGTCTGCG 18
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Db 14 CCCGAGGAGCACTGGC 31

RESULT 22
LOCUS 192481/c
DEFINITION Sequence 1 from patent US 5728526.
ACCESSION 192481
VERSION 192481.1 GI:3936951
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 800)
AUTHORS George A.L. Jr., Bhatnagar S.K. and Nazarenko, I.
TITLES Method for analyzing a nucleotide sequence
JOURNAL Patent: US 5728526-A 1 17-MAR-1998;
FEATURES
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1..800
/organism="unknown"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGAGGAGCACTGGC 18
Db 108 CCCGAGGAGCACTGGC 91

RESULT 23
LOCUS 122243/c
DEFINITION Sequence 13 from patent US 5527676.
ACCESSION 122243
VERSION 122243.1 GI:1602597
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1303)
AUTHORS Vogelstein, B., Baker, S.J., Fearon, E.R. and Nigro, J.M.
TITLES Detection of loss of the wild-type P53 gene and kits therefor
JOURNAL Patent: US 5527676-A 13 18-JUN-1996;
FEATURES
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Query Match 100.0%; Score 18; DB 6; Length 1303;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGAGGAGCACTGGC 18
Db 113 CCCGAGGAGCACTGGC 96

RESULT 24
LOCUS AX006172/c
DEFINITION Sequence 4 from Patent WO9904266.
ACCESSION AX006172
VERSION AX006172.1 GI:9929052
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1

AUTHORS Smith, G.C. and Jackson, S.P.
TITLES Assays, therapeutic methods and means
JOURNAL Patent: WO 9904266-A 4 28-JAN-1999;
SMITH GRAEME CAMERON MURRAY (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES
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1..1303
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 1303;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGAGGAGCACTGGC 18
Db 113 CCCGAGGAGCACTGGC 96

RESULT 25
LOCUS BD073938/c
DEFINITION Assay, remedy and remedy means.
ACCESSION BD073938
VERSION BD073938.1 GI:22619541
KEYWORDS JP 2001510684-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1303)
AUTHORS Lane, D.P., Jackson, S.P., Lakin, N.D. and Smith, G.C.M.
TITLES Assay, remedy and remedy means
JOURNAL Patent: JP 2001510684-A 2 07-AUG-2001;
KUDOS PHARMACEUTICALS LTD
OS Homo sapiens (human)
PN JP 2001510684-A/2
PD 07-AUG-2001
PF 16-JUL-1998 JP 2000503426
PR 16-JUL-1997 GB 9714971.0
PI DAVID PHILIP LANE, STEVEN PHILIP JACKSON, NICHOLAS DAVID LAKIN,
GRAHAM CAMERON MURRAY SMITH
PC C12N15/09, A61K38/00, A61P43/00, C07K14/82, C12N9/12, G01N33/15, PC
G01N33/50,
PC G01N33/566, C12N15/00, A61K37/02
CC Assay, remedy and remedy means
FH Key
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1..1303
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGAGGAGCACTGGC 18
Db 113 CCCGAGGAGCACTGGC 96

RESULT 26
LOCUS H00TP53B/c
DEFINITION Human p53 cellular tumor antigen mRNA, complete cds.
ACCESSION M14695
VERSION M14695.1 GI:339815
KEYWORDS antigen.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Bukacynska, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates, Catarrhini; Homnidae; Homo. 1 (bases 1 to 1303) Harris,N., Brill,E., Shohat,O., Prokocimer,M., Wolf,D., Arai,N. and Rottier,V.
TITLE	Molecular basis for heterogeneity of the human p53 protein
JOURNAL	Mol. Cell. Biol. 6 (12), 4650-4656 (1986)
MEDLINE	87089826
PUBMED	3025664
COMMENT	Original source text: Human transformed cell line SV-80, cDNA to mRNA, clone p53-H-19.
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ORIGIN	553 bp upstream of PuII site; chromosome 17p13.
Query Match	100.0%; Score 18; DB 9; Length 1303;
Best Local Similarity	100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Dy	1 CCCCGAAGGAGACTGTGC 18 113 CCCC GAAGGAGACTGTGC 96
RESULT 27	
LOCUS	122242 1307 bp DNA linear PAT 07-OCT-1996
DEFINITION	Sequence 12 from patent US 5527676.
ACCESSION	122242
VERSION	122242.1 GI:1602596
KEYWORDS	.
ORGANISM	Unknown.
SOURCE	Unclassified.
REFERENCE	1 (bases 1 to 1307)
AUTHORS	Vogelstein,B.; Baker,S.J., Pearson,E.R. and Nigro,J.M.
TITLE	Detection of loss of the wild-type P53 gene and kites therefor
JOURNAL	Patent: US 5527676-A 12 18-JUN-1996;
FEATURES	Location/Qualifiers 1..1307 /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Query Match	100.0%; Score 18; DB 6; Length 1307;
Best Local Similarity	100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Dy	1 CCCCCAAGGAGACTGTGC 18

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Db          117 CCGGAGAGCAGTCTGC 100

RESULT 28
LOCUS      HUMTP53a      1307 bp      mRNA      linear      PRI 14-JAN-1995
DEFINITION Human p53 cellular tumor antigen mRNA, complete cds.
ACCESSION  M14694
VERSION     M14694.1
KEYWORDS    GI:339813
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1307)
AUTHORS     Harris,N., Brill,E., Shohat,O., Prokocimer,M., Wolf,D., Arai,N. and
            Rotter,Y.
TITLE       Molecular basis for heterogeneity of the human p53 protein
JOURNAL     Mol. Cell. Biol. 6 (12), 4650-4656 (1986)
MEDLINE     87089826
PUBMED      3025664
COMMENT      Original source text: Human transformed cell line SV-80, cDNA to
            mRNA, clone p53-H-1
FEATURES
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            126..1307
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            /translation="MEEPQSDPSVEPPISQETFFSDLWKLPENNVLSPLSQANDDIM
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            CRRPRRTRESENIAKGEPRHPELPQSTRAALPNTSSSPQKKKPLDGEYFQIAG
            RRRFERELNEALELKDQADGKEPGSRHSHSLKSKGQSTSHKKLAKITGPDUS
            D"
ORIGIN      557 bp upstream of PvuII site; chromosome 17p13.
            Query Match      100.0%; Score 18; DB 9; Length 1307;
            Best Local Similarity 100.0%; Prd. No. 3.8e+02;
            Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy          1 CCGGAGAGCAGTCTGCG 18
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Db          117 CCGGAGAGCAGTCTGCG 100

RESULT 29
LOCUS      A67149/c      1317 bp      DNA      linear      PAT 29-MAR-1999
DEFINITION Sequence 6 from Patent WO9741433.
ACCESSION  A67149
VERSION     A67149.1
KEYWORDS    GI:4538506
SOURCE      unidentified
            unidentified
            unclassified.
            1 (bases 1 to 1317)
REFERENCE   Kouzarides,T.
TITLE       METHOD AND MEANS FOR DISRUPTION OF p53 AND RB INTERACTION
JOURNAL     Patent: WO 9741433-A 6 06-NOV-1997,
            CANCER RES CAMPAIGN TECH (GB)
FEATURES
    Location/Qualifiers

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RESULT 34	189361/c	1317 bp	DNA	linear	PAT 10-AUG-1998
LOCUS	189361				
DEFINITION	Sequence 1 from patent US 5721340.				
ACCESSION	189361				
VERSION	189361.1				
KEYWORDS	GI:3409301				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1317)				
TITLE	Halazonetis,T.D.				
JOURNAL	p33 proteins with altered tetramerization domains				
FEATURES	Patent: US 5721340-A 1 24-FEB-1998;				
source	Location/Qualifiers				
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Best Local Similarity	100.0%; Pred. No. 3.8e+02;				
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
CY	1 CCCGGAAGGCGAGCTGGC 18				
Db	127 CCCGGAAGGCGAGCTGGC 110				
RESULT 35	AR181303	1317 bp	DNA	linear	PAT 20-APR-2002
LOCUS	AR181303/c				
DEFINITION	Sequence 8 from patent US 6335164.				
ACCESSION	AR181303				
VERSION	AR181303.1				
KEYWORDS	GI:20223517				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1317)				
TITLE	Kigawa,K., Yamamaka,M., Kusumi,K., Mukai,E. and Obata,K.				
JOURNAL	Methods for targeting, enriching, detecting and/or isolating target				
FEATURES	nucleic acid sequence using RecA-like recombinase				
source	Patent: US 6335164-A 8 01-JAN-2002;				
	Location/Qualifiers				
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Best Local Similarity	100.0%; Pred. No. 3.8e+02;				
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
CY	1 CCCGGAAGGCGAGCTGGC 18				
Db	127 CCCGGAAGGCGAGCTGGC 110				
RESULT 36	AR218593	1317 bp	MRNA	linear	PAT 25-SEP-2002
LOCUS	AR218593/c				
DEFINITION	Sequence 1 from patent US 6420118.				
ACCESSION	AR218593				
VERSION	AR218593.1				
KEYWORDS	GI:23319373				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1317)				
TITLE	Halazonetis,T. and Hartwig,W.				
	Peptides and peptidomimetics with structural similarity to human				

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JOURNAL      p53 that activate p53 function
FEATURES
source       Patent: US 642018-A 1 16-JUN-2002;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        |||
        127 CCCGGAAGGCACTCGGC 110

RESULT 37
LOCUS       AX057140/c      1317 bp      DNA      PAT 17-JAN-2001
DEFINITION  Sequence 16 from Patent WO0075184.
ACCESSION   AX057140
VERSION     AX057140.1 GI:12309961
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS     Zhang,H., Tsveltkov,I.M. and Kondo,T.
TITLE       Modulation of protein levels using the scf complex
JOURNAL     Patent: WO 0075184-A 16 14-DEC-2000;
            YALE UNIVERSITY (US)
FEATURES
source      Location/Qualifiers
            1..1317
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            136..1317
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3,8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        127 CCCGGAAGGCACTCGGC 110

RESULT 38
LOCUS       AX203243/c      1317 bp      DNA      linear      PAT 30-AUG-2001
DEFINITION  Sequence 96 from Patent WO0153529.
ACCESSION   AX203243
VERSION     AX203243.1 GI:15392615
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
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FT /cell_type='bone marrow-derived cell' FT
FT CDS 215..1396
FT /product='mutated p53'
FT mutation replace(957,'g')
FT mutation replace(1317,'a')
FT Location/Qualifiers
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/db_xref='taxon:9606'

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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGAAGGAGCTCTGGC 18
Db 206 CCCGGAAGGAGCTCTGGC 189

RESULT 42
E13737/c 1760 bp DNA linear PAT 27-APR-1998
LOCUS CDNA encoding human p53 protein which is as p53 cancer inhibitory
DEFINITION gene product.
E13737
ACCESSION E13737.1 GI:3252505
VERSION UP 1997229933-A/1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1760)
Sugano, K. and Sacotte, K.
REFERENCE AUTANTIBODY DETECTING METHOD FOR P53 PROTEIN
AUTHORS Patent: JP 1997229933-A 1 05-SEP-1997;
JOURNAL SUGANO KOKICHI, NICHIREI CORP
COMMENT OS Homo sapiens (human)
PN JP 1997229933-A/1
PD 05-SEP-1997
PF 27-FEB-1996 UP 1996124123
PI SUGANO KOKICHI, SAOTOME KEIICHI
PC G01N33/53, C07K14/47, C07K16/42, G01N33/564;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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FT /organism='Homo sapiens'
FT /cell_line='WI-38VA13'
FT 5'UTR 1..214
FT CDS 215..1396
FT /product='Human p53 protein which is as p53
FT cancer
FT inhibitory gene product'
FT 3'UTR 1397..1760.
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGAAGGAGCTCTGGC 18
Db 206 CCCGGAAGGAGCTCTGGC 189

RESULT 43
BD084820/c 1760 bp DNA linear PAT 27-AUG-2002
LOCUS Diagnosis method and reagents.
DEFINITION BD084820
ACCESSION BD084820.1 GI:22630430
VERSION UP 2001522241-A/13.
KEYWORDS JP 2001522241-A/13.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1760)
Leeuwen, F.W.V., Grosveld, F.G. and Burbach, V.P.H.
REFERENCE Diagnosis method and reagents
AUTHORS Patent: JP 2001522241-A 13 13-NOV-2001;
JOURNAL ROYAL NETHERLANDS ACADEMY OF ARTS AND SCIENCES, ERASMUS UNIVERSITY
ROTTERDAM, UNIVERSITY OF UTRECHT
COMMENT OS Homo sapiens (human)
PN UP 2001522241-A/13
PD 13-NOV-2001
PF 02-APR-1998 JP 1998542545
PI 10-APR-1997 US 60/043163
PI FREDERIK W VAN LEEUWEN, FRANKLIN G GROSVELD, JOHANNES PETER
HENRI BURBACH
PC C12Q1/68, C07K14/47, C12N15/52, C12N9/00, C12N5/10, A61K38/43, PC
A01K67/027,
PC A01K48/00/C07K16/18
CC Strandedness: Double;
CC topology: Linear;
CC p53 cellular tumor antigen gene; Genbank accession number CC
K03199
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source
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 206 CCCGGAAGGAGCTCTGGC 189

RESULT 44
HUMP53T/c 1760 bp mRNA linear PRI 07-JAN-1995
LOCUS Human p53 cellular tumor antigen mRNA, complete cds.
DEFINITION HUMP53T
ACCESSION HUMP53T.1 GI:189478
VERSION K03199.1
KEYWORDS antigen; antigen p53.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1760)
Harlow, E.
REFERENCE Unpublished (1985)

```

REFERENCE AUTHORS      2 (bases 1 to 1760)
TITLE                  Harlow E., Williamson N.M., Ralston R., Helfman D.M. and Adams T.E.
JOURNAL MEDLINE        Molecular cloning and in vitro expression of a cDNA clone for human p53 cellular tumor antigen p53
PUBMED                Mol. Cell. Biol. 5 (7), 1601-1610 (1985)
AUTHORS               MCBride O.W., Merry D. and Givol D.
TITLE                 The gene for human p53 cellular tumor antigen is located on chromosome 17 short arm (17p13)
JOURNAL MEDLINE       Proc. Natl. Acad. Sci. U.S.A. 83 (1), 130-134 (1986)
PUBMED                86094327
COMMENT              Original source text : Human vulva carcinoma (cell line A431), cDNA to mRNA, clone p4-2..
                      [3] sites; chromosomal location.
                      A draft entry and sequence for [2], [1] were kindly submitted via electronic mail by E.Harlow 17-OCT-1985. [1] reports that positions 1-79 may be a cloning artifact generated by ligating a second, unrelated cDNA to the 5' end of the p53 CDNA.
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ORIGIN               1 bp upstream of SalI site; Chromosome 17p13 [Unpublished (1985) C. Query Match
Best Local Similarity 100.0%; Score 18; DB 9; Length 1760; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY          1 CCCGAAGCGACGCTGC 18
                                |||
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Db           206 CCCGAAGCAGCTGCC 189
RESULT 45 AF192534     2355 bp   DNA linear SYN 19-APR-20000
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DEFINITION Expression vector Ad5CMV-p53 tumor suppressor protein p53 (p53)
VERSION    AF192534
KEYWORDS   expression cassette, complete sequence.
SOURCE     Organism
ORGANISM   Expression vector Ad5CMV-p53
REFERENCE  Zhang W.W., Fang,X., Branch,C.D., Mazur,W., French,B.A. and Roth,J.A. Artificial sequences; vectors.
            1 (bases 1 to 2355)
            Geneth.U.A.
            Description and identification of recombinant adenovirus by

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FEATURES	source	gene	CDS	ORIGIN
JOURNAL	lipo-some-mediated transfection and PCR analysis			
MEDLINE	Biotechniques 15 (5), 868-872 (1993)			
PUBMED	94092464			
REFERENCE	8267983			
AUTHORS	2 (bases 1 to 2355)			
TITLE	Zhang, W.W., Fang, X., Mazur, W., French, B.A., Georges, R.N. and Roth, J.A.			
JOURNAL	High-efficiency gene transfer and high-level expression of wild-type p53 in human lung cancer cells mediated by recombinant adenovirus			
MEDLINE	Cancer Gene Ther. 1 (1), 5-13 (1994)			
PUBMED	95346687			
REFERENCE	7621238			
AUTHORS	3 (bases 1 to 2355)			
TITLE	Huet, T., Wilson, D.R., Zhang, W.W. and Roth, J.A.			
JOURNAL	Direct Submission			
MEDLINE	Submitted (05-OCT-1999) Oncology, Rhone-Poulenc Rorer Gencell, 38235			
PUBMED	Bay Center Place, Hayward, CA 94545, USA			
REFERENCE	Location/Qualifiers			
AUTHORS	1..2355			
TITLE	/organism="Expression vector Ad5CMV-p53"			
JOURNAL	/mol_type="Genomic DNA"			
MEDLINE	/db_xref="taxon:120786"			
PUBMED	/note="p53 expression cassette of RPR/INGN 201 recombinant			
REFERENCE	adenovirus vector. Artificial sequence, contains CMV			
AUTHORS	promoter and the SV40 polyadenylation signal"			
TITLE	921..2102			
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MEDLINE	921..2102			
PUBMED	/gene="p53"			
REFERENCE	/codon_start=1			
AUTHORS	/product="Tumor suppressor protein p53"			
TITLE	/protein_id="NAF64408.1"			
JOURNAL	/db_xref="GI:7595312"			
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REFERENCE	YQSGAPRLGSLGSGTAKSVCTCYSPALNKKMCOIAKCPQVLAWSNPFGTVERAM			
AUTHORS	ALTKQSCMTFVVARCCHHRCCSDSGILAPPGHILRYEENLAEVLYIDRMTFRSSVIV			
TITLE	PEPEVSSDCCTTHIVYCNSSCMGKMRPLITITLDESSGMLRNSFEVRCAC			
JOURNAL	CPGRARLTSEENLARKGEPRHELPGSTRALPNNITSSPQPKKPLDGEYFTLIQIGK			
MEDLINE	RRERFERELNEALELKDQAGKREPGSRASHSHLKSXKQGSTSHRKLMEKTGPPDS			
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REFERENCE				

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CM nucleic - nucleic search, using sw model

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Searched: 235373 seqs, 180373377 residues

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SUMMARIES

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4	18	100.0	1307	15	US-10-397-635-6
5	18	100.0	1307	9	US-09-732-384-8
6	18	100.0	1317	10	US-09-829-922-1
7	18	100.0	1317	14	US-10-160-290-1
8	18	100.0	1760	10	US-09-849-602-9
9	18	100.0	1760	15	US-10-191-121-4
10	18	100.0	2209	15	US-10-062-674-2065
11	18	100.0	2521	15	US-10-429-802-25
12	18	100.0	2521	15	US-10-430-503-16
13	18	100.0	2625	12	US-10-391-068-1
14	18	100.0	2629	14	US-10-077-176-58
15	18	100.0	2629	14	US-10-077-176-59

C 16	18	100.0	2629	14	US-10-077-176-60	Sequence 60, Appl
C 17	18	100.0	2629	14	US-10-077-176-61	Sequence 61, Appl
C 18	18	100.0	2629	15	US-10-439-388-16	Sequence 16, Appl
C 19	18	100.0	2629	15	US-10-165-216-3	Sequence 3, Appl
C 20	18	100.0	2629	15	US-10-159-563-188	Sequence 188, Appl
C 21	16.4	91.1	436	10	US-09-918-995-36880	Sequence 36880, A
C 22	16.4	91.1	905	14	US-10-066-543-113	Sequence 113, Appl
C 23	16.4	91.1	942	9	US-09-764-847-1845	Sequence 1845, Ap
C 24	16.4	91.1	942	9	US-09-764-847-1846	Sequence 1846, Ap
C 25	16.4	91.1	942	14	US-10-092-154-1845	Sequence 1845, Ap
C 26	16.4	91.1	942	14	US-10-092-154-1846	Sequence 1846, Ap
C 27	16.4	91.1	1866	9	US-09-765-231A-2	Sequence 2, Appl
C 28	15.4	85.6	184	9	US-09-884-441-332	Sequence 332, Appl
C 29	15.4	85.6	184	10	US-09-907-969-332	Sequence 332, Appl
C 30	15.4	85.6	184	10	US-09-827-271-332	Sequence 332, Appl
C 31	15.4	85.6	184	14	US-10-198-053-332	Sequence 332, Appl
C 32	15.4	85.6	358	15	US-10-242-535A-47690	Sequence 47890, A
C 33	15.4	85.6	371	15	US-10-242-535A-21425	Sequence 21425, A
C 34	15.4	85.6	395	15	US-10-242-535A-9459	Sequence 9459, Ap
C 35	15.4	85.6	399	15	US-10-242-535A-23153	Sequence 23153, A
C 36	15.4	85.6	400	15	US-10-242-535A-23042	Sequence 23042, A
C 37	15.4	85.6	400	15	US-10-242-535A-23133	Sequence 23133, A
C 38	15.4	85.6	405	9	US-09-922-217-755	Sequence 755, Appl
C 39	15.4	85.6	405	9	US-09-833-263-755	Sequence 755, Appl
C 40	15.4	85.6	405	13	US-10-025-380-755	Sequence 755, Appl
C 41	15.4	85.6	422	15	US-10-242-535A-58222	Sequence 58222, A
C 42	15.4	85.6	443	15	US-10-242-535A-17255	Sequence 17255, A
C 43	15.4	85.6	447	9	US-09-736-457-1634	Sequence 1634, Ap
C 44	15.4	85.6	447	9	US-09-902-941-1634	Sequence 1634, Ap
C 45	15.4	85.6	447	9	US-09-849-626-1634	Sequence 1634, Ap
C 46	15.4	85.6	447	14	US-10-017-754-1634	Sequence 1634, Ap
C 47	15.4	85.6	447	14	US-10-113-872-1634	Sequence 1634, Ap
C 48	15.4	85.6	460	15	US-10-242-535A-21058	Sequence 21058, A
C 49	15.4	85.6	460	15	US-10-242-535A-21058	Sequence 24495, A
C 50	15.4	85.6	460	15	US-10-242-535A-57305	Sequence 57305, A
C 51	15.4	85.6	472	15	US-10-242-535A-24508	Sequence 24508, A
C 52	15.4	85.6	496	15	US-10-242-535A-51996	Sequence 51996, A
C 53	15.4	85.6	500	15	US-10-242-535A-51996	Sequence 51996, A
C 54	15.4	85.6	500	15	US-10-242-535A-57271	Sequence 57271, A
C 55	15.4	85.6	500	15	US-10-242-535A-44600	Sequence 46000, A
C 56	15.4	85.6	500	15	US-10-027-832-126478	Sequence 126478, A
C 57	15.4	85.6	569	15	US-10-242-535A-48062	Sequence 48062, A
C 58	15.4	85.6	569	15	US-10-242-535A-48062	Sequence 48062, A
C 59	15.4	85.6	633	15	US-10-242-535A-45679	Sequence 45679, A
C 60	15.4	85.6	633	15	US-09-871-161-206	Sequence 206, Appl
C 61	15.4	85.6	634	15	US-10-242-535A-46209	Sequence 46209, A
C 62	15.4	85.6	647	9	US-09-604-287A-81	Sequence 81, Appl
C 63	15.4	85.6	647	9	US-09-339-338-81	Sequence 81, Appl
C 64	15.4	85.6	647	10	US-09-551-621-81	Sequence 81, Appl
C 65	15.4	85.6	647	13	US-10-007-805-81	Sequence 81, Appl
C 66	15.4	85.6	647	14	US-10-076-622-81	Sequence 81, Appl
C 67	15.4	85.6	647	14	US-10-124-805-81	Sequence 81, Appl
C 68	15.4	85.6	647	15	US-10-441-893-81	Sequence 81, Appl
C 69	15.4	85.6	723	12	US-10-282-122A-14650	Sequence 14650, A
C 70	15.4	85.6	755	15	US-10-264-049-1042	Sequence 1042, Ap
C 71	15.4	85.6	1280	12	US-10-282-122A-20383	Sequence 20383, A
C 72	15.4	85.6	1490	9	US-09-925-301-158	Sequence 158, Appl
C 73	15.4	85.6	1717	10	US-09-960-706-553	Sequence 553, Appl
C 74	15.4	85.6	1717	10	US-09-873-319-623	Sequence 623, Appl
C 75	15.4	85.6	1717	14	US-10-171-311-118	Sequence 118, Appl
C 76	15.4	85.6	1717	14	US-10-301-882-108	Sequence 108, Appl
C 77	15.4	85.6	1722	14	US-10-210-180-68	Sequence 68, Appl
C 78	15.4	85.6	1804	14	US-10-176-553-177	Sequence 177, Appl
C 79	15.4	85.6	1804	15	US-10-155-638-165	Sequence 365, Appl
C 80	15.4	85.6	1826	14	US-10-105-668-878	Sequence 878, Appl
C 81	15.4	85.6	1889	12	US-10-422-114-35157	Sequence 35157, A
C 82	15.4	85.6	2875	14	US-10-101-510-364	Sequence 364, Appl
C 83	15.4	85.6	2876	5	US-10-067-093A-1963	Sequence 1963, Ap
C 84	15.4	83.3	215	9	US-09-294-067B-1015	Sequence 3015, Ap
C 85	15.4	83.3	3112	12	US-10-422-114-22028	Sequence 22028, A
C 86	15.4	83.3	169139	14	US-10-067-514-1	Sequence 1, Appl
C 87	15.4	83.3	169139	15	US-10-419-123-1	Sequence 1, Appl
C 88	14.8	82.2	108	14	US-10-123-807-21	Sequence 21, Appl

89 14.8 82.2 563 15 US-10-027-632-84156 Sequence 84156, A
90 14.8 82.2 617 15 US-10-027-632-261398 Sequence 261398,
91 14.8 82.2 617 15 US-10-027-632-261399 Sequence 261399,
92 14.8 82.2 617 15 US-10-027-632-261400 Sequence 261400,
93 14.8 82.2 727 15 US-10-027-632-50560 Sequence 50560, A
94 14.8 82.2 730 15 US-10-027-632-13823 Sequence 13823, A
95 14.8 82.2 820 15 US-10-027-632-168125 Sequence 168125,
96 14.8 82.2 820 15 US-10-027-632-168126 Sequence 168126,
97 14.8 82.2 820 15 US-10-027-632-168127 Sequence 168127,
98 14.8 82.2 823 15 US-10-027-632-168128 Sequence 168128,
99 14.8 82.2 823 15 US-10-027-632-128849 Sequence 128849,
100 14.8 82.2 838 15 US-10-027-632-172737 Sequence 172737,

ALIGNMENTS

RESULT 1
US-09-848-868-35
Sequence 35, Application US/09848868
Publication No. US20030166588A1
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick L.
TITLE OF INVENTION: Splice-Region Antisense Composition and
FILE REFERENCE: 0450-0037.30
CURRENT APPLICATION NUMBER: US/09/848, 868
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/202,376
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense
US-09-848-868-35

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTGTGCG 18
DB 1 CCGGAGGCGAGTGTGCG 18

RESULT 2
US-09-848-868-36
Sequence 36, Application US/09848868
Publication No. US20030166588A1
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick L.
TITLE OF INVENTION: Splice-Region Antisense Composition and
FILE REFERENCE: 0450-0037.30
CURRENT APPLICATION NUMBER: US/09/848, 868
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/202,376
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense
US-09-848-868-36

Query Match 100.0%; Score 18; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTGTGCG 18
DB 17 CCGGAGGCGAGTGTGCG 34

RESULT 3
US-09-776-695-22/c
Sequence 22, Application US/09776695
Patent No. US20020068283A1
GENERAL INFORMATION:
APPLICANT: Boeke, Jef
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
MUTATIONS WHICH SUPPRESS P53 CANCER MUTA- TIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner & Wilcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776, 695
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,006
FILING DATE: 2001-03-28
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-776-695-22

Query Match 100.0%; Score 18; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTGTGCG 18
DB 35 CCGGAGGCGAGTGTGCG 18

RESULT 4
US-10-397-635-6/c
Sequence 6, Application US/10397635
Publication No. US2004000604A1
GENERAL INFORMATION:
APPLICANT: ZHANG, XIAOLIU
APPLICANT: FU, XUPING
TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER

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/ TITLE OF INVENTION: THERAPY
/ FILE REFERENCE: P02410US2
/ CURRENT APPLICATION NUMBER: US/10/397,635
/ CURRENT FILING DATE: 2003-03-26
/ PRIOR APPLICATION NUMBER: 60/357,788
/ PRIOR FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: 60/410,024
/ PRIOR FILING DATE: 2002-09-11
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 1303
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-397-635-6

Query Match 100.0%; Score 18; DB 15; Length 1303;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
/ | | | | | | | | | | | | | | | | | |
/ | | | | | | | | | | | | | | | | | |
/ 113 CCCGGAAGGCGAGTCTGGC 96

Db 113 CCCGGAAGGCGAGTCTGGC 96

RESULT 5
US-09-732-384-8/c
/ Sequence 8, Application US/09732384
/ Patent No. US20020132977A1
/ GENERAL INFORMATION:
/ APPLICANT: Yuan, Zhi-Min
/ TITLE OF INVENTION: Inhibition of p53 Degradation
/ FILE REFERENCE: 21508-044
/ CURRENT APPLICATION NUMBER: US/09/732,384
/ CURRENT FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: 60/769,816
/ PRIOR FILING DATE: 1999-12-08
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 1307
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-732-384-8

Query Match 100.0%; Score 18; DB 9; Length 1307;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
/ | | | | | | | | | | | | | | | | | |
/ | | | | | | | | | | | | | | | | | |
/ 117 CCCGGAAGGCGAGTCTGGC 100

Db 117 CCCGGAAGGCGAGTCTGGC 100

RESULT 6
US-09-829-922-1/c
/ Sequence 1, Application US/09829922
/ Publication No. US20030171537A1
/ GENERAL INFORMATION:
/ APPLICANT: Halazonetis, Thanos
/ TITLE OF INVENTION: Peptides and peptidomimetics with
/ structural similarity to human p53 that activate p53
/ TITLE OF INVENTION: Function
/ FILE REFERENCE: 2973.19998
/ CURRENT APPLICATION NUMBER: US/09/829,922
/ CURRENT FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: 08/894,327
/ PRIOR FILING DATE: 1997-12-04
/ PRIOR APPLICATION NUMBER: pctx96/01535
/ PRIOR FILING DATE: 1996-02-16
/ PRIOR APPLICATION NUMBER: 08/392,542

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PRIORITY FILING DATE: 1995-02-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1317
TYPE: DNA
ORGANISM: Homo sapiens
US-09-829-922-1

Query Match
Best Local Similarity 100.0%; Score 18; DB 10; Length 1317;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 CCCGAGGCGACTGTGGC 18
127 CCCGAGGCGACTGTGGC 110

RESULT 7
US-10-160-290-1/c
Sequence 1, Application US/10160290
Publication No. US20030124557v1
GENERAL INFORMATION:
APPLICANT: Halazoneis, Tanos
Hartwig, Wolfgang
TITLE OF INVENTION: Peptides and Peptidomimetics with
Structural Similarity to Human p53 That Activate
p53
NUMBER OF SEQUENCES: 35
FUNCTION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/160,290
FILING DATE: 04-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/685,027
FILING DATE: 10-Oct-2000
APPLICATION NUMBER: 08/392,542
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486-48439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-160-290-1

Query Match
Best Local Similarity 100.0%; Score 18; DB 14; Length 1317;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```


QY 1 CCGGAGGAGCAGTCTGGC 18
|||
Db 127 CCGGAGGAGCAGTCTGGC 110

RESULT 8
US-09-849-602-9/c
; Sequence 9, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105 (JW)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-849-602-9

Query Match 100.0%; Score 18; DB 10; Length 1760;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCAGTCTGGC 18
|||
Db 206 CCGGAGGAGCAGTCTGGC 189

RESULT 9
US-10-191-121-4/c
; Sequence 4, Application US/10191121
; Publication No. US20040005574A1
; GENERAL INFORMATION:
; APPLICANT: Guarente, Leonard
; APPLICANT: Vaziri, Homayoun
; APPLICANT: Imai, Shin-Ichiro
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: Sir2 and p53 Deacetylation
; FILE REFERENCE: 13407-015002
; CURRENT APPLICATION NUMBER: US/10/191,121
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US 60/303,456
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 10/NNN,NNN
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: US 60/303,370
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-121-4

Query Match 100.0%; Score 18; DB 15; Length 1760;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCAGTCTGGC 18
|||
Db 206 CCGGAGGAGCAGTCTGGC 189

RESULT 10

US-10-062-674-2065/c
; Sequence 2065, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 2065
; LENGTH: 2209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 430224.2
US-10-062-674-2065

Query Match 100.0%; Score 18; DB 15; Length 2209;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCAGTCTGGC 18
|||
Db 170 CCGGAGGAGCAGTCTGGC 153

RESULT 11
US-10-429-802-25/c
; Sequence 25, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: WONG, KA YIN
; APPLICANT: ZOU, YIYU
; TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
; FILE REFERENCE: UTSQ:752US
; CURRENT APPLICATION NUMBER: US/10/429,802
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/377,672
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 2521
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-429-802-25

Query Match 100.0%; Score 18; DB 15; Length 2521;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCAGTCTGGC 18
|||
Db 127 CCGGAGGAGCAGTCTGGC 110

RESULT 12
US-10-430-503-16/c
; Sequence 16, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LAN, KENG-LI
; APPLICANT: OU-YANG, FU
; APPLICANT: LIU, JAW-CHING
; APPLICANT: LAN, KENG-HSIN
; TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC

```

; TITLE OF INVENTION: REAGENTS
; FILE REFERENCE: UTSC:797US
; CURRENT APPLICATION NUMBER: US/10/430,503
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/383,063
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 2521
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-430-503-16

Query Match          100.0%; Score 18; DB 15; Length 2521;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCACTCTGAC 18
Db 127 CCGGAGGCACTCTGAC 110

RESULT 13
US-10-391-068-1/c
; Sequence 1, Application US/10391068
; Publication No. US20040028654A1
; GENERAL INFORMATION:
; APPLICANT: JI, LIN
; APPLICANT: ROTH, JACK
; TITLE OF INVENTION: PROTAMINE-ADENOVIIRAL VECTOR COMPLEXES
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: INRP:097US
; CURRENT APPLICATION NUMBER: US/10/391,068
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/366,846
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURS:
; NAME/KEY: CDS
; LOCATION: (252) ..(1433)
US-10-391-068-1

Query Match          100.0%; Score 18; DB 12; Length 2625;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCACTCTGAC 18
Db 243 CCGGAGGCACTCTGAC 226

RESULT 14
US-10-077-176-58/c
; Sequence 59, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008
; CURRENT APPLICATION NUMBER: US/10/077,176
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
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US-10-077-176-58

Query Match          100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCACTCTGAC 18
Db 243 CCGGAGGCACTCTGAC 226

RESULT 15
US-10-077-176-59/c
; Sequence 59, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008
; CURRENT APPLICATION NUMBER: US/10/077,176
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-176-59

Query Match          100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCACTCTGAC 18
Db 243 CCGGAGGCACTCTGAC 226

RESULT 16
US-10-077-176-60/c
; Sequence 60, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008
; CURRENT APPLICATION NUMBER: US/10/077,176
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-176-60

Query Match          100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCACTCTGAC 18
Db 243 CCGGAGGCACTCTGAC 226

RESULT 17
US-10-077-176-61/c
; Sequence 61, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008
```

;; CURRENT APPLICATION NUMBER: US/10/077,176
;; CURRENT FILING DATE: 2002-02-19
;; NUMBER OF SEQ ID NOS: 71
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 61
;; LENGTH: 2629
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-077-176-61

Query Match 100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 243 CCCGAGGCGAGTCTGGC 226

RESULT 18
US-10-439-388-16/C
;; Sequence 16, Application US/10439388
;; Publication No. US20030228617A1
;; GENERAL INFORMATION:
;; APPLICANT: Aune, Thomas M
;; APPLICANT: Olsen, Nancy J
;; TITLE OF INVENTION: Method for Predicting Autoimmune Disease
;; FILE REFERENCE: 1242/58
;; CURRENT APPLICATION NUMBER: US/10/439,388
;; CURRENT FILING DATE: 2003-05-16
;; PRIOR APPLICATION NUMBER: US 60/381,055
;; PRIOR FILING DATE: 2002-05-16
;; NUMBER OF SEQ ID NOS: 70
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 16
;; LENGTH: 2629
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-439-388-16

Query Match 100.0%; Score 18; DB 15; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 243 CCCGAGGCGAGTCTGGC 226

RESULT 19
US-10-165-216-3/C
;; Sequence 3, Application US/10165216
;; Publication No. US20030228675A1
;; GENERAL INFORMATION:
;; APPLICANT: Oterness, Diane M.
;; APPLICANT: Abraham, Robert T.
;; TITLE OF INVENTION: ATM Related Kinase Aty, Nucleic Acids
;; FILE REFERENCE: P-LJ 5222
;; CURRENT APPLICATION NUMBER: US/10/165,216
;; CURRENT FILING DATE: 2002-06-06
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 2629
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (252)...(1433)
US-10-165-216-3

Query Match 100.0%; Score 18; DB 15; Length 2629;

Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 243 CCCGAGGCGAGTCTGGC 226

RESULT 20
US-10-159-563-188/C
;; Sequence 188, Application US/10159563
;; Publication No. US20040009154A1
;; GENERAL INFORMATION:
;; APPLICANT: Khan, Javed
;; APPLICANT: Ringner, Markus
;; APPLICANT: Peterson, Carsten
;; APPLICANT: Meltzer, Paul
;; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
;; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
;; FILE REFERENCE: 11613.56US11
;; CURRENT APPLICATION NUMBER: US/10/159,563
;; CURRENT FILING DATE: 2002-12-09
;; PRIOR APPLICATION NUMBER: US 10/133,937
;; PRIOR FILING DATE: 2002-04-25
;; NUMBER OF SEQ ID NOS: 444
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 188
;; LENGTH: 2629
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-159-563-188

Query Match 100.0%; Score 18; DB 15; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 243 CCCGAGGCGAGTCTGGC 226

RESULT 21
US-09-918-995-36880/C
;; Sequence 36880, Application US/09918995
;; Publication No. US20030073623A1
;; GENERAL INFORMATION:
;; APPLICANT: Hyseq, Inc.
;; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
;; FILE REFERENCE: 20411-756
;; CURRENT APPLICATION NUMBER: US/09/918,995
;; CURRENT FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: US/09/235,076
;; PRIOR FILING DATE: 1999-01-20
;; NUMBER OF SEQ ID NOS: 38054
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 36880
;; LENGTH: 436
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-918-995-36880

Query Match 91.1%; Score 16.4; DB 10; Length 436;
Best Local Similarity 94.4%; Pred. No. 55;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 90 CCCGAGGCGAGTCTGGC 73

RESULT 22
US-10-066-543-113/C

```
/ Sequence 113, Application US/10066543
/ Publication No. US20030087818A1
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Yudi
/ APPLICANT: Pyle, Ruth A.
/ APPLICANT: Xu, Jianshun
/ APPLICANT: Indrias, Carol Joseph
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Secrist, Heather
/ APPLICANT: Carter, Darick
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Smith, Carole L.
/ APPLICANT: Durham, Margalita
/ APPLICANT: Stolk, John A.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
/ FILE REFERENCE: 210121.563
/ CURRENT APPLICATION NUMBER: US/10/066,543
/ CURRENT FILING DATE: 2002-01-31
/ NUMBER OF SEQ ID NOS: 3417
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 113
/ LENGTH: 905
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: 13, 45, 386, 545, 580, 582, 584, 590, 591, 603, 606, 609,
/ LOCATION: 610, 616, 621, 623, 624, 625, 629, 630, 646, 652, 670, 672,
/ LOCATION: 674, 676, 688, 700, 709, 710, 744, 753, 756, 758, 759, 763,
/ LOCATION: 786, 796, 823, 851, 876, 885
/ OTHER INFORMATION: n = A, T, C or G
US-10-066-543-113

Query Match          91.1%; Score 16.4; DB 14; Length 905;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 516 CCCGAGGCGAGTCTGGC 499

RESULT 23
US-09-764-847-1845/C
/ Sequence 1845, Application US/09764847
/ Patent No. US20020132767A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC009
/ CURRENT APPLICATION NUMBER: US/09/764,847
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - consult PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 2003
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1845
/ LENGTH: 942
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-764-847-1845

Query Match          91.1%; Score 16.4; DB 9; Length 942;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 CCCGAGGCGAGTCTGGC 18
DB 58 CCCGAGGCGAGTCTGTC 41
```

RESULT 24
US-09-764-847-1846/C

```
/ Sequence 1846, Application US/09764847
/ Patent No. US20020132767A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC009
/ CURRENT APPLICATION NUMBER: US/09/764,847
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - consult PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 2003
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1846
/ LENGTH: 942
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-764-847-1846
```

```
Query Match          91.1%; Score 16.4; DB 9; Length 942;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 CCCGAGGCGAGTCTGGC 18
DB 58 CCCGAGGCGAGTCTGTC 41
```

```
RESULT 25
US-10-092-154-1845/C
/ Sequence 1845, Application US/10092154
/ Publication No. US20030054375A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC009C1
/ CURRENT APPLICATION NUMBER: US/10/092,154
/ CURRENT FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 2003
/ Prior application removed - See File Wrapper or Palm
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1845
/ LENGTH: 942
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-092-154-1845
```

```
Query Match          91.1%; Score 16.4; DB 14; Length 942;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CCCGAGGCGAGTCTGGC 18
DB 58 CCCGAGGCGAGTCTGTC 41
```

Search completed: March 2, 2004, 04:51:58
Job time : 273 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 21:35:15 ; Search time 48 Seconds
(without alignments)

208.107 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 cccggaagcagctcggc 18

Scoring table: IDENTITY NUC

Gapop 10-0, Gapexc 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database: Issued Patents NA:*

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2: /cgn2_6/ptodata/2/ina/6A COMB.seg:*

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4: /cgn2_6/ptodata/2/ina/6C COMB.seg:*

5: /cgn2_6/ptodata/2/ina/6D COMB.seg:*

6: /cgn2_6/ptodata/2/ina/backfile1.seg:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	102	1	US-08-047-041A-15
2	18	100.0	133	1	US-08-047-041A-12
3	18	100.0	133	2	US-08-795-006A-22
4	18	100.0	133	3	US-09-184-073-22
5	18	100.0	800	1	US-08-472-239-1
6	18	100.0	1070	3	US-09-414-436-4
7	18	100.0	1303	1	US-08-047-041A-13
8	18	100.0	1307	1	US-08-047-041A-12
9	18	100.0	1317	1	US-07-912-011-1
10	18	100.0	1317	1	US-08-347-792-1
11	18	100.0	1317	1	US-08-431-357-1
12	18	100.0	1317	2	US-08-697-221-1
13	18	100.0	1317	3	US-08-392-542-1
14	18	100.0	1317	3	US-08-894-327-1
15	18	100.0	1317	4	US-08-147-751-8
16	18	100.0	1317	4	US-09-305-914-1
17	18	100.0	1317	4	US-09-685-027-1
18	18	100.0	1317	5	PCT-US95-15353-1
19	15.4	85.6	184	4	US-09-404-879A-332
20	15.4	85.6	447	4	US-09-702-705-1634
21	15.4	85.6	447	4	US-09-736-457-1634
22	15.4	85.6	447	4	US-09-614-124B-1634
23	15.4	85.6	447	4	US-09-671-325-1634
24	15.4	85.6	633	3	US-09-385-982-206
25	15.4	85.6	647	4	US-09-222-575-81
26	15.4	85.6	647	4	US-09-389-681-81
27	15.4	85.6	647	4	US-09-620-405B-81
28	15.4	85.6	647	4	US-09-339-338-81
29	15.4	85.6	647	4	US-09-433-826B-81
30	15.4	85.6	647	4	US-09-604-287A-81
31	15.4	85.6	647	4	US-09-285-480-81
32	15.4	85.6	647	4	US-09-834-758-81
33	15.4	85.6	647	4	US-08-447-179-7
34	14.8	82.2	108	1	US-09-445-247-21
35	14.8	82.2	1757	5	US-08-094-071-1
36	14.8	82.2	1757	5	PCT-US92-00878-1
37	14.8	82.2	8078	3	US-08-870-126-12
38	14.8	82.2	14985	1	US-09-445-247-12
39	14.8	82.2	14985	1	US-08-652-972A-6
40	14.8	82.2	14985	5	PCT-US96-06231A-6
41	14.8	82.2	4403765	3	US-09-103-840A-2
42	14.8	82.2	4411529	3	US-09-103-840A-1
43	14.4	80.0	252	4	US-09-621-976-11048
44	14.4	80.0	360	1	US-08-256-077-3
45	14.4	80.0	360	1	US-08-466-127-3
46	14.4	80.0	982	1	US-08-256-077-1
47	14.4	80.0	982	1	US-08-466-127-1
48	14.4	80.0	8137	4	US-09-566-921-7
49	13.8	76.7	157	3	US-08-721-986-1
50	13.8	76.7	157	3	US-08-225-487A-1
51	13.8	76.7	212	1	US-08-435-684A-28
52	13.8	76.7	212	1	US-08-934-877A-28
53	13.8	76.7	212	3	US-08-871-678C-28
54	13.8	76.7	237	4	US-09-552-931A-10772
55	13.8	76.7	371	4	US-08-585-593A-35
56	13.8	76.7	441	4	US-08-914-375C-53
57	13.8	76.7	579	4	US-09-404-879A-188
58	13.8	76.7	579	4	US-09-338-933-188
59	13.8	76.7	579	4	US-09-215-681-188
60	13.8	76.7	579	4	US-09-216-003A-188
61	13.8	76.7	584	4	US-09-404-879A-187
62	13.8	76.7	584	4	US-09-338-933-187
63	13.8	76.7	584	4	US-09-215-681-187
64	13.8	76.7	584	4	US-09-216-003A-187
65	13.8	76.7	627	1	US-09-489-039A-2235
66	13.8	76.7	630	1	US-08-527-227A-5
67	13.8	76.7	635	1	US-09-643-597-208
68	13.8	76.7	635	4	US-09-480-884A-208
69	13.8	76.7	655	4	US-09-542-615A-208
70	13.8	76.7	655	4	US-09-606-421B-208
71	13.8	76.7	690	4	US-09-328-352-3319
72	13.8	76.7	732	4	US-09-886-319A-54
73	13.8	76.7	771	4	US-09-328-352-3448
74	13.8	76.7	844	1	US-08-166-195A-1
75	13.8	76.7	844	1	US-08-436-775-1
76	13.8	76.7	854	1	US-08-436-883B-1
77	13.8	76.7	855	4	US-09-252-991A-10688
78	13.8	76.7	859	4	US-09-894-844-46
79	13.8	76.7	987	4	US-09-252-991A-15247
80	13.8	76.7	993	4	US-09-833-381-895
81	13.8	76.7	1001	4	US-09-671-311-230
82	13.8	76.7	1001	4	US-09-671-311-231
83	13.8	76.7	1032	4	US-09-016-433-1338
84	13.8	76.7	1116	4	US-09-252-991A-15444
85	13.8	76.7	1290	4	US-09-107-532A-3539
86	13.8	76.7	1344	4	US-09-252-991A-15551
87	13.8	76.7	1355	4	US-09-489-039A-439
88	13.8	76.7	1355	4	US-09-252-991A-11115
89	13.8	76.7	1403	2	US-08-202-044-1
90	13.8	76.7	1403	2	US-08-751-344B-1
91	13.8	76.7	1403	4	US-09-920-868A-1
92	13.8	76.7	1403	3	US-09-255-366-1
93	13.8	76.7	1413	4	US-09-252-991A-11233
94	13.8	76.7	1446	4	US-09-252-991A-10948
95	13.8	76.7	1474	1	US-08-466-980-1
96	13.8	76.7	1474	2	US-09-053-303-1
97	13.8	76.7	1474	2	US-09-339-115-1
98	13.8	76.7	1474	5	PCT-US95-17093-1
99	13.8	76.7	1633	4	US-09-061-154-1
100	13.8	76.7	1633	4	US-09-061-154-3

ALIGNMENTS

RESULT 1
US-08-047-041A-15/c
Sequence 15, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047, 041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928, 661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446, 584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330, 566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107, 42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: exon 2
PUBLICATION INFORMATION:
AUTHORS: Lamb,
JOURNAL: Mol. Cell. Biol.
VOLUME: 6
ISSUE: 5
PAGES: 1379-1385
DATE: 1986
US-08-047-041A-15

Query Match 100.0%; Score 18; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.8;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCGGAGGAGCTCTGCG 18
Db 20 CCGGAGGAGCTCTGCG 3

RESULT 2
US-08-047-041A-2/c
Sequence 2, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047, 041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928, 661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446, 584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330, 566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107, 42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: exon 2
PUBLICATION INFORMATION:
AUTHORS: Buchman, V. L.
TITLE: A variation in the structure of the
JOURNAL: Gene
VOLUME: 70
PAGES: 245-252
DATE: 1986
US-08-047-041A-2

Query Match 100.0%; Score 18; DB 1; Length 133;

Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTGTGGC 18
DB 35 CCCGAGGAGCTGTGGC 18

RESULT 3

US-08-795-006A-22/c
Sequence 22, Application US/08795006A
Patent No. 5840579

GENERAL INFORMATION:

APPLICANT: Boeke, Jef
APPLICANT: Brachmann, Rainer
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
TITLE OF INVENTION: MUTATIONS WHICH SUPPRESS P53 CANCER MUTATIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,006A
FILING DATE: 05-FEB-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299

TELEX:

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-795-006A-22

Query Match

Best Local Similarity 100.0%; Score 18; DB 2; Length 133;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTGTGGC 18
DB 35 CCCGAGGAGCTGTGGC 18

RESULT 4

US-09-184-073-22/c
Sequence 22, Application US/09184073
Patent No. 6183964

GENERAL INFORMATION:

APPLICANT: Boeke, Jef
APPLICANT: Brachmann, Rainer
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
TITLE OF INVENTION: MUTATIONS WHICH SUPPRESS P53 CANCER MUTATIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

ADDRESSER: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,073
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/795,006

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299

TELEX:

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-184-073-22

Query Match

Best Local Similarity 100.0%; Score 18; DB 3; Length 133;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTGTGGC 18
DB 35 CCCGAGGAGCTGTGGC 18

RESULT 5

US-08-472-239-1/c
Sequence 1, Application US/08472239
Patent No. 5728526

GENERAL INFORMATION:

APPLICANT: GEORGE, Jr., Albert L.
APPLICANT: BHATNAGAR, Satish K.
APPLICANT: NAZARENKO, Irena
TITLE OF INVENTION: METHOD FOR ANALYZING A NUCLEOTIDE
TITLE OF INVENTION: SEQUENCE AND KIT THEREFOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATTHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,239
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mukai, Robert G.
REGISTRATION NUMBER: 28,531

REFERENCE/DOCKET NUMBER: 020160-229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-472-239-1

Query Match 100.0%; Score 18; DB 1; Length 800;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCAGCTGTGC 18
DB 108 CCCGGAAGGCAGCTGTGC 91

RESULT 6
US-09-414-436-4/c
Sequence 4, Application US/09414436
Patent No. 6294384
GENERAL INFORMATION:
APPLICANT: Dell'Acqua, Giorgio
APPLICANT: Mann, Michael J.
TITLE OF INVENTION: Compositions and Methods Based Upon an Isoform of p53
FILE REFERENCE: p53f
CURRENT APPLICATION NUMBER: US/09/414,436
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: 60/103,849
EARLIER FILING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1070
TYPE: DNA
ORGANISM: Homo sapiens
US-09-414-436-4

Query Match 100.0%; Score 18; DB 3; Length 1070;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCAGCTGTGC 18
DB 127 CCCGGAAGGCAGCTGTGC 110

RESULT 7
US-08-047-041A-13/c
Sequence 13, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
MAP POSITION: 17p13.1
PUBLICATION INFORMATION:
AUTHORS: Harris, N.
JOURNAL: Mol. Cell. Biol
VOLUME: 6
ISSUE: 12
PAGES: 4650-4656
DATE: 1986
US-08-047-041A-13

Query Match 100.0%; Score 18; DB 1; Length 1303;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCAGCTGTGC 18
DB 113 CCCGGAAGGCAGCTGTGC 96

RESULT 8
US-08-047-041A-12/c
Sequence 12, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20001.4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/047.041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
MAP POSITION: 17p13.1
PUBLICATION INFORMATION:
AUTHORS: Harris, N.
TITLE: Molecular basis for heterogeneity of the
TITLE: human p53 protein
JOURNAL: Mol. Cell. Biol.
VOLUME: 6
ISSUE: 12
PAGES: 4650-4656
DATE: 1986
US-08-047-041A-12

Query Match 100.0%; Score 18; DB 1; Length 1307;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 117 CCGGAGGCGAGTCTGGC 100

RESULT 9
US-07-912-011-1/c
Sequence 1, Application US/07912011
Patent No. 5382510
GENERAL INFORMATION:
APPLICANT: Levine, Arnold J.
APPLICANT: Shenk, Thomas E.
APPLICANT: Finlay, Cathy A.
TITLE OF INVENTION: Probes for Detecting Mutant p53
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSES: Imclone Systems Incorporated
STREET: 180 Varlick Street
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/07/912.011
FILING DATE: 10-JUL-1992
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/912,011
FILING DATE: 10-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEV-1-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-912-011-1

Query Match 100.0%; Score 18; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 127 CCGGAGGCGAGTCTGGC 110

RESULT 10
US-08-347-792-1/c
Sequence 1, Application US/08347792
Patent No. 5573925
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: P53 Proteins With Altered
TITLE OF INVENTION: Tetramerization Domains
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSES: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/347,792
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST58USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
US-08-347-792-1

Query Match 100.0%; Score 18; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
DB 127 CCCGGAAGCAGCTGGC 110

RESULT 11

US-08-431-357-1/c
Sequence 1, Application US/08431357
Patent No. 5721340

GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
TITLE OF INVENTION: Tetramerization Domains
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST58USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
US-08-431-357-1

Query Match 100.0%; Score 18; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
DB 127 CCCGGAAGCAGCTGGC 110

RESULT 12
US-08-697-221-1/c
Sequence 1, Application US/08697221
Patent No. 5847083

GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: Modified p53 Constructs and Uses
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,221
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,802
FILING DATE: 22-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST64AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
US-08-697-221-1

Query Match 100.0%; Score 18; DB 2; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
DB 127 CCCGGAAGCAGCTGGC 110

RESULT 13

US-08-392-542-1/c
Sequence 1, Application US/08392542
Patent No. 6169073

GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
TITLE OF INVENTION: Peptides and Peptidomimetics with
TITLE OF INVENTION: Structural Similarity to Human p53 That Activate p53
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.

```

;
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,542
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske, Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 0486,48439
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9100
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-392-542-1
;
Query Match 100.0%; Score 18; DB 3; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGGAGGCGAGCTGTGC 18
Db 127 CCGGAGGCGAGCTGTGC 110

RESULT 14
; Sequence 1, Application US/08894327
; Patent No. 6245886
; GENERAL INFORMATION:
; APPLICANT: Halazonec, Thanos
; TITLE OF INVENTION: peptides and peptidomimetics with
; TITLE OF INVENTION: structural similarity to human p53 that activate p53
; FILE REFERENCE: 2973,19998
; CURRENT APPLICATION NUMBER: US/08/894,327
; CURRENT FILING DATE: 1997-12-04
; EARLIER APPLICATION NUMBER: pctus96/01535
; EARLIER FILING DATE: 1996-02-16
; EARLIER APPLICATION NUMBER: 08/392,542
; EARLIER FILING DATE: 1995-02-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-08-894-327-1
;
Query Match 100.0%; Score 18; DB 3; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGGAGGCGAGCTGTGC 18
Db 127 CCGGAGGCGAGCTGTGC 110

RESULT 15
US-09-147-751-8/c
```

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; Sequence 8, Application US/09147751
; Patent No. 6335164
; GENERAL INFORMATION:
; APPLICANT: KIGAWA, Koji
; APPLICANT: YANAKA, Mikayo
; APPLICANT: KUSUMI, Kayo
; APPLICANT: MUKAI, Eli
; APPLICANT: OBATA, Kazuaki
; TITLE OF INVENTION: METHODS FOR TARGETING, ENRICHING,
; TITLE OF INVENTION: DETECTING AND/OR ISOLATING TARGET NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: USING REG- LIKE RECOMBINASE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,751
; FILING DATE: 18-MAY-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP97/03019
; FILING DATE: 29-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8/347090
; FILING DATE: 26-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8/229061
; FILING DATE: 23-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Maebius, Stephen B.
; REGISTRATION NUMBER: 35,264
; REFERENCE/DOCKET NUMBER: 8435/108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
;
US-09-147-751-8
;
Query Match 100.0%; Score 18; DB 4; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGGAGGCGAGCTGTGC 18
Db 127 CCGGAGGCGAGCTGTGC 110

RESULT 16
US-09-305-914-1/c
; Sequence 1, Application US/09305914
; Patent No. 638062
; GENERAL INFORMATION:
; APPLICANT: Halazonec, Thanos D.
; APPLICANT: Stavridi, Elena S.
; TITLE OF INVENTION: Modified p53 Tetramerization Domains Having Hydrophobic
; FILE REFERENCE: WST84AUSA
; CURRENT APPLICATION NUMBER: US/09/305,914
```

CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: 60/084,839
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1
LENGTH: 1317
TYPE: DNA
ORGANISM: human p53
FEATURE:
NAME/KEY: CDS
LOCATION: (136)..(1314)
US-09-305-914-1

Query Match 100.0%; Score 18; DB 4; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 127 CCGGAGGCGAGTCTGGC 110

RESULT 17
US-09-685-027-1/c
Sequence 1, Application US/09685027
Patent No. 6420118
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
Hartwig, Wolfgang
TITLE OF INVENTION: Peptides and Peptidomimetics with
Structural Similarity to Human p53 That Activate p53
Function
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/685,027
FILING DATE: 10-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,542
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486,48439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-685-027-1

Query Match 100.0%; Score 18; DB 4; Length 1317;

Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 127 CCGGAGGCGAGTCTGGC 110

RESULT 18
PCT-US95-15353-1/c
Sequence 1, Application PC/TUS9515353
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy
and Biology
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
TITLE OF INVENTION: Tetramerization Domains
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15353
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/431,357
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/456,623
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST58CPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
PCT-US95-15353-1

Query Match 100.0%; Score 18; DB 5; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 127 CCGGAGGCGAGTCTGGC 110

RESULT 19
US-09-404-879A-332

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; Sequence 332, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-404-879A-332
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Query Match 85.6%; Score 15.4; DB 4; Length 184;
Best Local Similarity 94.1%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 CCGAAGGCGAGTCTGGC 18
DB 112 CCGAAGGCGAGTCTGGC 128
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```
RESULT 20
US-09-702-705-1634/C
; Sequence 1634, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1634
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-702-705-1634
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```
Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 2 CCGAAGGCGAGTCTGGC 18
DB 73 CCGAAGGCGAGTCTGGC 57
```

```
RESULT 21
US-09-736-457-1634/C
; Sequence 1634, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
US-09-736-457-1634
```

```
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1634
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1634
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```
Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 CCGAAGGCGAGTCTGGC 18
DB 73 CCGAAGGCGAGTCTGGC 57
```

```
RESULT 22
US-09-614-124B-1634/C
; Sequence 1634, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1634
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-614-124B-1634
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```
Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 CCGAAGGCGAGTCTGGC 18
DB 73 CCGAAGGCGAGTCTGGC 57
```

```
RESULT 23
US-09-671-325-1634/C
; Sequence 1634, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
US-09-671-325-1634
```

```

; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1634
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-671-325-1634
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```

Query Match      85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      2 CCGAAGGAGCTCTGGC 18
Db      73 CCGAAGGAGCTCTGGC 57
```

```

RESULT 24
US-09-385-982-206/C
; Sequence 206, Application US/09385982
; Patent No. 6262314
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDDA-260X
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(633)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-206
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```

Query Match      85.6%; Score 15.4; DB 3; Length 633;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      2 CCGAAGGAGCTCTGGC 18
Db      426 CCGAAGGAGCTCTGGC 410
```

```

RESULT 25
US-09-222-575-81
; Sequence 81, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yagiu, Jiang
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
```

```

; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Human
; US-09-222-575-81
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Query Match      85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      2 CCGAAGGAGCTCTGGC 18
Db      575 CCGAAGGAGCTCTGGC 591
```

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Search completed: March 2, 2004, 03:48:42
Job time : 54 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 23:55:06 ; Search time 2529 Seconds

(without alignments)
212.542 Million cell updates/sec

Title: us-09-848-868-35

Perfect score: 18

Sequence: 1 cccggaagcagctcggc 18

Scoring table: IDENTITY NUC

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Maximum Match 100%
Listing first 200 summaries

EST:*

1: em_estba:*
2: em_estbm:*
3: em_estbn:*
4: em_estbu:*
5: em_estbv:*
6: em_estbl:*
7: em_estro:*
8: em_estc:*
9: gb_estl:*
10: gb_est2:*
11: gb_estc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_dln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mus:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rpd:*
26: em_gss_phg:*
27: em_gss_vit:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	190	9	AU076984 AU076984
2	18	100.0	203	9	AA296373 EST10934
3	18	100.0	230	14	CB117906 CB117906
4	18	100.0	234	14	H97230 H97230 yx04g12.r1

5	18	100.0	360	12	BG257442 BG257442
6	18	100.0	401	10	AM407968 UI-HF-BM0
7	18	100.0	494	14	CB149902 K-EST0206
8	18	100.0	478	12	BM834910 K-EST0110
9	18	100.0	513	9	AU129655 AU129655
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11	18	100.0	537	14	CB135305 K-EST0187
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13	18	100.0	540	14	CB150761 K-EST0207
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15	18	100.0	575	9	AU280602 AU280602
16	18	100.0	590	12	BM788930 K-EST0067
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18	18	100.0	592	12	BM849478 K-EST0129
19	18	100.0	602	12	BM833776 K-EST0108
20	18	100.0	606	12	BM764147 K-EST0045
21	18	100.0	606	12	BM772261 K-EST0056
22	18	100.0	612	14	CB138393 K-EST0191
23	18	100.0	622	10	BM613913 601504033
24	18	100.0	633	9	AU131823 AU131823
25	18	100.0	649	14	CB134750 K-EST0186
26	18	100.0	657	12	BM390105 602415946
27	18	100.0	682	12	B1832854 603082033
28	18	100.0	688	9	AU121050 AU121050
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30	18	100.0	707	12	BM011389 603635585
31	18	100.0	723	9	AU141723 AU141723
32	18	100.0	724	9	AU131952 AU131952
33	18	100.0	726	12	BM012402 603636972
34	18	100.0	729	9	AU141300 AU141300
35	18	100.0	732	12	BM048582 603623927
36	18	100.0	744	12	BE273022 601173343
37	18	100.0	750	12	BM048815 603628360
38	18	100.0	758	12	B1839950 603083048
39	18	100.0	762	13	BM462478 BM462478
40	18	100.0	765	12	BM044564 603622210
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48	18	100.0	818	13	BM0224113 AGENCOURT
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50	18	100.0	847	9	AU139600 AU139600
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52	18	100.0	871	12	BM106488 602289885
53	18	100.0	887	13	BM386866 BM386866
54	18	100.0	890	13	BM092819 AGENCOURT
55	18	100.0	897	13	BM0942658 AGENCOURT
56	18	100.0	898	13	BM0508407 AGENCOURT
57	18	100.0	905	9	AU130707 AU130707
58	18	100.0	905	13	BM0959887 AGENCOURT
59	18	100.0	907	13	BM0229042 AGENCOURT
60	18	100.0	913	10	BM032445 602298141
61	18	100.0	916	9	AL520820 AL520820
62	18	100.0	917	10	BM342477 602013985
63	18	100.0	923	13	BM0919242 AGENCOURT
64	18	100.0	924	18	B1917918 603181673
65	18	100.0	927	12	BM327832 602426845
66	18	100.0	927	13	BM165476 AGENCOURT
67	18	100.0	930	12	BM046196 603625863
68	18	100.0	936	13	BM0894209 AGENCOURT
69	18	100.0	937	13	BM0925820 AGENCOURT
70	18	100.0	941	12	B1518429 603062136
71	18	100.0	949	13	BM0277633 AGENCOURT
72	18	100.0	963	12	BM338735 602436583
73	18	100.0	972	12	BM423840 602436583
74	18	100.0	975	10	BM797075 602257924
75	18	100.0	977	13	BM0923115 AGENCOURT
76	18	100.0	992	13	BM0214218 AGENCOURT
77	18	100.0	1005	13	BM0931123 AGENCOURT

C 78	18	100.0	1060	13	BU157354	AGENCOURT	C 151	15.4	85.6	424	12	B1817349	GI-F5 Axi
C 79	18	100.0	1087	12	BG338352	602436132	C 152	15.4	85.6	424	14	W30204	W30204 mc26d10.r1
C 80	18	100.0	1089	12	BM466114	AGENCOURT	C 153	15.4	85.6	427	14	CP11695	CP11695 Shu1xom1
C 81	18	100.0	1123	10	BE900862	601673833	C 154	15.4	85.6	428	9	A1909705	A1909705 PM-BT20-
C 82	18	100.0	1201	13	AL530477	AL530477	C 155	15.4	85.6	428	14	R58670	R58670 G4595 Fetal
C 83	18	100.0	1201	13	BX345594	BX345594	C 156	15.4	85.6	436	9	A1759475	A1759475 E15STea28
C 84	18	100.0	1333	12	BM469215	AGENCOURT	C 157	15.4	85.6	439	10	BP115709	BP115709 uc37loc7.Y
C 85	17.6	97.8	998	9	AL521702	AL521702	C 158	15.4	85.6	440	12	BQ94809	BQ94809 PMO-BN017
C 86	17.6	94.4	416	9	AA177861	AA177861	C 159	15.4	85.6	452	9	AL036065	AL036065 DKF2P56F
C 87	17	94.4	737	13	AA1735141	AA1735141	C 160	15.4	85.6	454	13	BY482752	BY482752 BX482752
C 88	17	94.4	1016	13	BX396796	BX396796	C 161	15.4	85.6	465	10	AM885823	AM885823 RC4-OT007
C 89	16.6	92.2	884	29	CNS02160	NS02160	C 162	15.4	85.6	470	10	BE106945	BE106945 UI-R-BT1-
C 90	16.6	91.1	268	9	AA298090	AA298090	C 163	15.4	85.6	478	12	BSG61196	BSG61196 PMO-CR082
C 91	16.4	91.1	303	14	R25957	R25957	C 164	15.4	85.6	478	14	CF790074	CF790074 B67418 MA
C 92	16.4	91.1	372	10	BF651887	BF651887	C 165	15.4	85.6	478	14	HO3678	HO3678 YJ42B11.r1
C 93	16.4	91.1	498	14	H50566	H50566	C 166	15.4	85.6	480	14	W49749	W49749 ZC41608.r1
C 94	16.4	91.1	513	10	BF043070	BF043070	C 167	15.4	85.6	483	10	AM630245	AM630245 hb8d07.Y
C 95	16.4	91.1	604	10	BF541984	BF541984	C 168	15.4	85.6	484	9	AA967116	AA967116 ua40e05.r
C 96	16.4	91.1	644	10	BE144316	BE144316	C 169	15.4	85.6	485	12	BT061083	BT061083 BU061083
C 97	16.4	91.1	685	12	BG432786	BG432786	C 170	15.4	85.6	487	13	BQ319870	BQ319870 PMO-CR082
C 98	16.4	91.1	697	12	BG294801	BG294801	C 171	15.4	85.6	485	10	AM885788	AM885788 RC4-OT007
C 99	16.4	91.1	723	12	BG621970	BG621970	C 172	15.4	85.6	497	9	AA111707	AA111707 mp08a11.r
C 100	16.4	91.1	740	9	BU139631	BU139631	C 173	15.4	85.6	497	10	BE106377	BE106377 UI-R-BT1-
C 101	16.4	91.1	790	12	BG212909	BG212909	C 174	15.4	85.6	503	10	BF567951	BF567951 UI-R-B00-
C 102	16.4	91.1	815	9	BU119965	BU119965	C 175	15.4	85.6	504	10	BE833812	BE833812 RC4-OT007
C 103	16.4	91.1	837	9	BU119797	BU119797	C 176	15.4	85.6	505	14	CF569008	CF569008 017-102-r
C 104	16.4	91.1	844	10	BF316085	BF316085	C 177	15.4	85.6	506	14	AA009423	AA009423 zeb3c08.r
C 105	16.4	91.1	856	13	BU146860	BU146860	C 178	15.4	85.6	506	14	CB723596	CB723596 UI-M-GK0-
C 106	16.4	91.1	861	9	BU118353	BU118353	C 179	15.4	85.6	509	10	AM673601	AM673601 ba5sh01.Y
C 107	16.4	91.1	876	12	BG455676	BG455676	C 180	15.4	85.6	510	10	AM520875	AM520875 UI-R-BUP
C 108	16.4	91.1	916	13	BQ919531	BQ919531	C 181	15.4	85.6	510	14	CB143418	CB143418 K-EST0197
C 109	16.4	91.1	931	12	B114676	B114676	C 182	15.4	85.6	511	12	B1817644	B1817644 G2-M6 Axi
C 110	16.4	91.1	942	9	BU117581	BU117581	C 183	15.4	85.6	514	9	AA184937	AA184937 mc88a02.r
C 111	16.4	91.1	1014	12	BG598893	BG598893	C 184	15.4	85.6	515	12	B1775888	B1775888 468609 MA
C 112	16.4	91.1	1038	10	BE786919	BE786919	C 185	15.4	85.6	518	28	AA296219	AA296219 PRC1-23-1
C 113	16.4	91.1	1040	12	BM644765	BM644765	C 186	15.4	85.6	521	10	AM838191	AM838191 QY2-LT005
C 114	16.4	91.1	1040	12	BQ436739	AGENCOURT	C 187	15.4	85.6	524	12	B1817305	B1817305 GI-D10 AX
C 115	16.4	91.1	1170	12	BM013221	600634947	C 188	15.4	85.6	530	12	BM721923	BM721923 UI-E-B00-
C 116	16.4	91.1	1170	12	BM013221	600634947	C 189	15.4	85.6	539	14	CB265876	CB265876 1004781 H
C 117	16	88.9	760	9	BF036211	DKF2P564H	C 190	15.4	85.6	540	12	BG537072	BG537072 602565158
C 118	16	88.9	978	10	BF309375	BF309375	C 191	15.4	85.6	545	9	AA177319	AA177319 EST220936
C 119	16	88.9	1201	13	EX355038	EX355038	C 192	15.4	85.6	550	9	AA277412	AA277412 vb69d11.r
C 120	15.4	85.6	105	10	AM388465	AM388465	C 193	15.4	85.6	555	10	BG643376	BG643376 uv67a06.Y
C 121	15.4	85.6	220	9	AV019229	AV019229	C 194	15.4	85.6	556	10	AM388278	AM388278 MR2-ST012
C 122	15.4	85.6	244	9	AA331081	EST34946	C 195	15.4	85.6	559	29	CC753990	CC753990 ZWMBB013
C 123	15.4	85.6	250	14	CB029906	TG8ETzyd1	C 196	15.4	85.6	562	14	CB266565	CB266565 1005471 H
C 124	15.4	85.6	269	9	AA360652	EST69891	C 197	15.4	85.6	564	9	AU280282	AU280282 AU280282
C 125	15.4	85.6	273	10	AM330252	EST33954	C 198	15.4	85.6	570	12	BG530001	BG530001 602558845
C 126	15.4	85.6	273	10	AM330252	EST33954	C 199	15.4	85.6	571	13	BO126161	BO126161 1114a07.Y
C 127	15.4	85.6	287	9	AA333978	EST36122	C 200	15.4	85.6	571	28	AA109510	AA109510 RPT1-23-4
C 128	15.4	85.6	292	12	B1015695	B1015695							
C 129	15.4	85.6	296	9	AI933573	AI933573							
C 130	15.4	85.6	299	9	AA328516	BY354672							
C 131	15.4	85.6	300	13	BY354672	BY354672							
C 132	15.4	85.6	324	9	AA358056	AA358056							
C 133	15.4	85.6	325	12	BG608755	BG608755							
C 134	15.4	85.6	361	14	CB270401	CB270401							
C 135	15.4	85.6	363	14	B1295366	B1295366							
C 136	15.4	85.6	375	14	R25637	R25637							
C 137	15.4	85.6	376	29	CG781817	1123026E1							
C 138	15.4	85.6	386	10	BF706710	28130 MA							
C 139	15.4	85.6	391	12	BG814972	dab98c10							
C 140	15.4	85.6	394	29	CG344533	CG64890TC							
C 141	15.4	85.6	395	29	CB776194	AMGNDC:S							
C 142	15.4	85.6	399	29	CG782144	1123046G0							
C 143	15.4	85.6	401	29	CG773386	CG773386							
C 144	15.4	85.6	402	29	CG782158	1123016E1							
C 145	15.4	85.6	404	13	C28802	C28802							
C 146	15.4	85.6	409	10	BB680161	BB680161							
C 147	15.4	85.6	409	12	BM482266	535083 MA							
C 148	15.4	85.6	409	28	AQ006068	CIT-HSP-2							
C 149	15.4	85.6	413	12	BM106200	509669 MA							
C 150	15.4	85.6	420	9	AA329660	EST33298							

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AU076984/c
 AU076984 Sugano cDNA library
 similar to 5'-end region of Human p53 cellular tumor antigen mRNA,
 mRNA sequence.

AU076984.1 GI:7439546
 Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 190)

Suzuki, Y., Ishihara, D., Sasaki, M., Nakagawa, H., Hata, H.,
 Tanoda, T., Watanabe, M., Komatsu, T., Ota, T., Isegaki, T., Suyama, A.
 and Sugano, S.
 Statistical analysis of the 5' untranslated region of human mRNA

JOURNAL
Genomics 64 (3), 286-297 (2000)
MEDLINE
20221373
PubMed
10756096
COMMENT

using 'Oligo-Capped' cDNA libraries
Department of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yasukik@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
This clone was obtained from a 'full length-enriched' cDNA library
constructed by 'Oligo-Capping' method. The coding region starts
from the 50 bp upstream to the 3'-end.
Location/Qualifiers
1..190
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano cDNA library"

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 190;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAAGGCGAGTCTGGC 18
|||||
Db 132 CCGGAAGGCGAGTCTGGC 115

RESULT 2
AA296373 203 bp mRNA linear EST 18-APR-1997
LOCUS EST10934 umbilical vein endothelial cells II Homo sapiens cDNA 5'
DEFINITION end similar to transformation-associated protein p53, mRNA
sequence.

ACCESSION
AA296373
VERSION AA296373.1 GI:1948779
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 203)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Feldner, R.A.,
Bult, C.J., Lee, N.H., Kirsch, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, M., C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fritch, W.M., Fritchman, J.L., Georghiou, N.S.,
Glock, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Keller, J.M., Kelley, J.C., Liu, L.-I., Marmaro, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,
Small, K.V., Sprague, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Peng, D.-P., Ferris, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kusch, C., Hung, J., Li, H., Welsner, F.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.

TITLE
JOURNAL
MEDLINE
PUBMED
9602680
Nature 377 (6547 Suppl.), 3-174 (1995)
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

COMMENT
Other ESTs: THC168370
Contact: Kerlavage, AR
Bioinformatics

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699483
Email: arkerlavage@igr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M3 Reverse.
Location/Qualifiers
1..203
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (insect):194290"
/db_xref="taxon:9606"
/cell_type="endothelial cell"
/dev_stage="fetus"
/clone_lib="Umbilical vein endothelial cells II"
/note="Organ: umbilical vein; Vector: pBluescript SK-";
Site_1: EcoRI; Site_2: XhoI"

FEATURES

Query Match 100.0%; Score 18; DB 9; Length 203;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAAGGCGAGTCTGGC 18
|||||
Db 118 CCGGAAGGCGAGTCTGGC 101

RESULT 3
CB117906 230 bp mRNA linear EST 28-JAN-2003
LOCUS K-EST0163962 B1T694954 Homo sapiens cDNA clone B1T694954-4-F11 5',
DEFINITION mRNA sequence.
ACCESSION
CB117906
VERSION CB117906.1 GI:27943713
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 230)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boseon-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: F column: 11
High quality sequence frop: 230.

TITLE
JOURNAL
COMMENT
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boseon-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: F column: 11
High quality sequence frop: 230.

FEATURES

Location/Qualifiers
1..230
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="B1T694954-4-F11"
/sex="M"
/lab_host="Top10F"
/clone_lib="B1T694954"
/note="Organ: Brain; Vector: pCNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first

strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for electroporation of competent cells E. coli Top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

Query Match 100.0%; Score 18; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 134 CCGGAGGCGAGTCTGGC 117

RESULT 4
H97230/c
LOCUS
DEFINITION
H97230 234 bp mRNA linear EST 11-DEC-1995
YX04912.t Soares melanocyte 2NDHM Homo sapiens cDNA clone
IMAGE:260806 5' similar to gb:XE4156_rnal CELLULAR TUMOR ANTIGEN
P53 (HUMAN) mRNA sequence.

ACCESSION
H97230
VERSION
H97230.1 GI:1114273
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 234)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE
The Mashu-Merck EST Project
JOURNAL
Unpublished (1995)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 2246 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

1. 234
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3870448"
/db_xref="taxon:9606"
/clone="IMAGE:260806"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NDHM"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker site 1. Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - Oligo(dT) primer [5'
TGTTACCATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albano."

Query Match 100.0%; Score 18; DB 14; Length 234;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 104 CCGGAGGCGAGTCTGGC 87

RESULT 5
BG257442/c
LOCUS
DEFINITION
BG257442 360 bp mRNA linear EST 13-FEB-2001
60237775F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4508539 5',
mRNA sequence.
ACCESSION
BG257442
VERSION
BG257442.1 GI:12767258
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 360)
NIH-MGC http://mgc.mcl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov

Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: IMAGE0387 row: e column: 20
High quality sequence stop: 360.
Location/Qualifiers

FEATURES

1. 360
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4508539"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 107 CCGGAGGCGAGTCTGGC 90

RESULT 6
AM407968/c
LOCUS
DEFINITION
AM407968 401 bp mRNA linear EST 16-FEB-2000
U1-HF-BX0-ad1-a-03-0-U1.r2 NIH_MGC_38 Homo sapiens cDNA clone
IMAGE:3061901 5', mRNA sequence.

ACCESSION AM407368
 VERSION AM407368.1 GI:6927025
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS 1 (bases 1 to 401)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-rc@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: www.bio.lmnl.gov/biopr/image/image.html
 Seq primer: M13 Forward

FEATURES

Source

Location/Qualifiers
 1..401
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3061901"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_id="NIH MGC 38"
 /note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (2.5-3.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fátima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCGGAAGCGAGCTGGC 18
 |||||||||
 DB 55 CCCGGAAGCGAGCTGGC 38

RESULT 7
 CBI49902/c CBI49902 434 bp mRNA linear EST 29-JAN-2003
 LOCUS K-EST0206507 L15CKX1 Homo sapiens cDNA clone L15CKX1-48-G06 5',
 DEFINITION mRNA sequence.
 ACCESSION CBI49902
 VERSION CBI49902
 KEYWORDS EST.
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 434)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr
 Plate: 48 row: G column: 06
 High quality sequence stop: 434.
 Location/Qualifiers
 1..434

FEATURES

Source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L15CKX1-48-G06"
 /sex="M"
 /cell_line="CK-K1"
 /lab_host="Top10F"
 /clone_id="L15CKX1"
 /note="Organ: liver; Vector: pCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deacapped with tabacco acid pyrophosphatase (TAP). The deacapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 434;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCGGAAGCGAGCTGGC 18
 |||||||||
 DB 131 CCCGGAAGCGAGCTGGC 114

RESULT 8
 BM834910/c BM834910 478 bp mRNA linear EST 06-MAR-2002
 LOCUS K-EST0110069 S11SNV1 Homo sapiens cDNA clone S11SNV1-51-E01 5',
 DEFINITION mRNA sequence.
 ACCESSION BM834910
 VERSION BM834910
 KEYWORDS EST.
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 478)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 51 row: E column: 01
 High quality sequence stop: 478.
 Location/Qualifiers
 1..478

FEATURES

Source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S11SNV1-51-E01"

/sex="M"
 /tissue_type="Stomach"
 /cell_type="Lymphoblast-like"
 /cell_line="SNU-1"
 /lab_host="Top10F"
 /clone_lib="S11SNU1"
 /note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII-digested pME18-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 478;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGACGACTGTGGC 18
 |||||
 Db 132 CCGGAGGACGACTGTGGC 115

RESULT 9
 AU129655/c 513 bp mRNA linear EST 01-AUG-2002
 LOCUS AU129655 NT2RP2 Homo sapiens cDNA clone NT2RP205982 5', mRNA
 DEFINITION AU129655 NT2RP2 Homo sapiens cDNA clone NT2RP205982 5', mRNA
 sequence.
 ACCESSION AU129655
 VERSION AU129655.1 GI:10990009
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 513)
 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,T., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
 HRI human cDNA project
 Unpublished (2000)
 CONTACT: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

Location/Qualifiers
 1..513
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NT2RP205982"
 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /clone_id="NT2RP2"
 /note="Vector: pME18FL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 513;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGACGACTGTGGC 18
 |||||
 Db 184 CCGGAGGACGACTGTGGC 167

RESULT 10
 BF794506/c 521 bp mRNA linear EST 12-JAN-2001
 LOCUS BF794506 NT1_MGC_65 Homo sapiens cDNA clone IMAGE:4339142 5',
 DEFINITION BF794506 NT1_MGC_65 Homo sapiens cDNA clone IMAGE:4339142 5',
 sequence.
 ACCESSION BF794506
 VERSION BF794506.1 GI:12099560
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 521)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: gga@remail.nih.gov
 Tissue Procurement: Louis Staudt, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Plate: LLM9949 row: c column: 15
 High quality sequence stop: 519.
 Location/Qualifiers
 1..521
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4339142"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC 85"
 /note="Organ: lymph; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."

FEATURES

Location/Qualifiers
 1..521
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4339142"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC 85"
 /note="Organ: lymph; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."

ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 521;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGACGACTGTGGC 18
 |||||
 Db 163 CCGGAGGACGACTGTGGC 146

RESULT 11
 CB135305/c 537 bp mRNA linear EST 29-JAN-2003
 LOCUS CB135305 K-EST0187411 LSHLK1 Homo sapiens cDNA clone LSHLK1-32-F04 5', mRNA
 DEFINITION K-EST0187411 LSHLK1 Homo sapiens cDNA clone LSHLK1-32-F04 5', mRNA
 sequence.
 ACCESSION CB135305
 VERSION CB135305.1 GI:28102030
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ORIGIN

REFERENCE

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 537)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 32 row: F column: 04
High quality sequence stop: 537.
Location/Qualifiers

COMMENT

FEATURES

Source

1. 537
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LSHLK1-32-F04"
/sex="M"
/cell_line="HLK-1"
/lab_host="Top10F"
/clone_1b="LSHLK1"
/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deacapped
with tabacco acid pyrophosphatase (TAP). The deacapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 537;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCGAGAGCAGCTGGC 18
|||||
Db 132 CCCGAGAGCAGCTGGC 115

RESULT 12
BM833945/c 538 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST010801 S11SN11 Homo sapiens cDNA clone S11SN11-59-A11 5',
DEFINITION mRNA sequence.
ACCESSION BM833945
VERSION BM833945.1 GI:19190354
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 538)
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 59 row: A column: 11
High quality sequence stop: 538.
Location/Qualifiers

FEATURES

Source

1. 538
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S11SN11-59-A11"
/sex="M"
/tissue_type="Stomach"
/cell_type="Lymphoblast-like"
/cell_line="SKO-1"
/lab_host="Top10F"
/clone_1b="S11SN11"
/note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI;
Site 2: XhoI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deacapped
with tabacco acid pyrophosphatase (TAP). The deacapped
intact mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dt primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with SfiI and
cloned into DraIII-digested pYES18-FL3 vector. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 538;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCGAGAGCAGCTGGC 18
|||||
Db 152 CCCGAGAGCAGCTGGC 135

RESULT 13
CB150761/c 540 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST020575 C11SN117 Homo sapiens cDNA clone C11SN117-34-H06 5',
DEFINITION mRNA sequence.
ACCESSION CB150761
VERSION CB150761.1 GI:28134341
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 540)
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 34 row: H column: 06
High quality sequence stop: 540.
Location/Qualifiers

FEATURES

source

1. 540

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CISNU17-34-H06"

/sex="F"

/tissue_type="uterine"

/cell_type="epithelial"

/cell_line="SNU-17"

/lab_host="top10f"

/clone_id="CISNU17"

/note="Organ: Cervix; Vector: PCNS-D2; Site:1: EcoRI; Site:2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deacapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli top10f, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 540;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGAGGCGAGTCTGGC 18

Db 133 CCGGAGGCGAGTCTGGC 116

RESULT 14

AU127286/c 554 bp mRNA linear EST 01-AUG-2002

LOCUS AU127286 NT2RP2 Homo sapiens cDNA clone NT2RP2000945 5', mRNA

DEFINITION sequence.

ACCESSION AU127286

VERSION AU127286.1 GI:10952002

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y., Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and Isogai.T.

HRI human cDNA project

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

Location/Qualifiers

1..554

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="NT2RP2000945"

/cell_type="teratocarcinoma"

/cell_line="NT2"

/clone_id="NT2RP2"

/note="Vector: PME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 554;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGAGGCGAGTCTGGC 18

Db 132 CCGGAGGCGAGTCTGGC 115

RESULT 15

AU280602/c 575 bp mRNA linear EST 31-JUL-2003

LOCUS AU280602 N18SE2 Homo sapiens cDNA clone N18SE2002780 5', mRNA

DEFINITION sequence.

ACCESSION AU280602

VERSION AU280602.1 GI:28299829

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 575)

Imabayashi.H., Mori.T., Gojo.S., Kiyono.T., Sugiyama.T., Irie.R., Isogai.T., Hata.J., Tomoya.Y. and Umezawa.A.

Redifferentiation of dedifferentiated chondrocytes and chondrogenesis of human bone marrow stromal cells via chondrosphere formation with expression profiling by large-scale cDNA analysis

Exp. Cell Res. 288 (1), 35-50 (2003)

22760698

12878157

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; Sugiyama.T., Wakamatsu.A., Irie.R., Umezawa.A., Fukuma.M., Kusakari.S., Hata.J., Ishii.S., Yamamoto.J., Isono.Y., Saito.K., Nakamura.Y., Masuno.Y., Nagai.K., Isogai.T.

HRI human cDNA project; cDNA library construction & 5'-end one pass sequencing: Helix Research Institute.

Location/Qualifiers

1..575

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="N18SE2002780"

/cell_type="mesenchymal stem cells"

/clone_id="N18SE2"

/note="Vector: PME18SFL3"

FEATURES

Location/Qualifiers

1..575

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="N18SE2002780"

/cell_type="mesenchymal stem cells"

/clone_id="N18SE2"

/note="Vector: PME18SFL3"

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 575;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGAGGCGAGTCTGGC 18

Db 132 CCGGAGGCGAGTCTGGC 115

RESULT 16

BW788590 590 bp mRNA linear EST 05-MAR-2002

LOCUS BW788590/c

DEFINITION K-EST0067764 S11SNU1 Homo sapiens cDNA clone S11SNU1-24-c03 5',

RNA sequence.

ACCESSION BM788590 GI:19136822

VERSION BM788590.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr

Plate: 24 row: G column: 03

High quality sequence stop: 590.

Location/Qualifiers

1..590

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S11SN01-24-G03"

/sex="M"

/tissue_type="Stomach"

/cell_type="Lymphoblast-like"

/cell_line="SNU-1"

/lab_host="Top10F"

/clone_lib="S11SN01"

/note="Origin: Stomach; Vector: pME18-F13; Site 1: XhoI; Site 2: XhoI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII-digested pMT18S-F13 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 590;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCGGAAGGCAAGTCTGCG 18

DB 131 CCCGGAAGGCAAGTCTGCG 114

RESULT 17

BM849186/c 590 bp mRNA linear EST 06-MAR-2002

LOCUS K-EST0129212 S13KMS5 Homo sapiens cDNA clone S13KMS5-66-B06 5',

DEFINITION mRNA sequence.

ACCESSION BM849186

VERSION BM849186.1 GI:19205585

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 590)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr

Plate: 66 row: E column: 06

High quality sequence stop: 590.

Location/Qualifiers

1..590

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S13KMS5-66-B06"

/tissue_type="myeloma"

/cell_line="KMS-5"

/lab_host="Top10F"

/clone_lib="S13KMS5"

/note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 590;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCGGAAGGCAAGTCTGCG 18

DB 132 CCCGGAAGGCAAGTCTGCG 115

RESULT 18

BM849478/c 592 bp mRNA linear EST 06-MAR-2002

LOCUS K-EST0129549 S13KMS5 Homo sapiens cDNA clone S13KMS5-69-A07 5',

DEFINITION mRNA sequence.

ACCESSION BM849478

VERSION BM849478.1 GI:19205877

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology

52 Eoenn-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krrib.re.kr
Plate: 69 row: A column: 07
High quality sequence stop: 592.
Location/Qualifiers
1..592

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-69-A07"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector: pcnS, Site_1: EcoRI, Site_2: NotI. The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 592;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGCTGTGCG 18
|||||
Db 132 CCCGAGGCGAGCTGTGCG 115

RESULT 19
BM833776/c 602 bp mRNA linear EST 06-MAR-2002
LOCUS BM833776
DEFINITION K-EST0108618 S13SNUI Homo sapiens cDNA clone S13SNUI-57-B08 5', mRNA sequence.
ACCESSION BM833776
VERSION BM833776.1 GI:19190185
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 602)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
TITLE 'Unpublished (2002)
JOURNAL
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoenn-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krrib.re.kr
Plate: 57 row: B column: 08
High quality sequence stop: 602.
Location/Qualifiers
1..602
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13SNUI-57-B08"
/sex="M"
/tissue_type="Stomach"
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/cell_line="SNU-1"
/lab_host="Top10F"
/clone_lib="S13SNUI"
/note="Organ: Stomach, Vector: pME18-Fl3, Site_1: XhoI, Site_2: XhoI. The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII-digested pME18-Fl3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 602;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGCTGTGCG 18
|||||
Db 134 CCCGAGGCGAGCTGTGCG 117

RESULT 20
BM764147/c 606 bp mRNA linear EST 04-MAR-2002
LOCUS BM764147
DEFINITION K-EST0045606 S13KMS5 Homo sapiens cDNA clone S13KMS5-23-E10 5', mRNA sequence.
ACCESSION BM764147
VERSION BM764147.1 GI:19093762
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 606)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
TITLE 'Unpublished (2002)
JOURNAL
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoenn-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krrib.re.kr
Plate: 23 row: E column: 10
High quality sequence stop: 606.
Location/Qualifiers
1..606
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-23-E10"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector: pcnS, Site_1: EcoRI, Site_2: NotI. The poly

(A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 606;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCCGAGGCGAGCTGGC 18
|||
Db 132 CCCGAGGCGAGCTGGC 115

RESULT 21
BM772261 606 bp mRNA linear EST 04-MAR-2002
LOCUS K-EST0056378 S13XMS561 Homo sapiens cDNA clone S13XMS561-1-B04 5',
DEFINITION mRNA sequence.
ACCESSION BM772261
VERSION BM772261.1 GI:19101876
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 606)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001

TITLE Unpublished (2002)
JOURNAL
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boseun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 1 row: B column: 04
High quality sequence stop: 606.
Location/Qualifiers
1. 606

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13XMS561-1-B04"
/tissue_type="myeloma"
/cell_line="RMS-5"
/lab_host="Top10⁺"
/clone_lib="S13XMS561"
/note="Vector: pCNS1; Site 1: EcoRI, Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is

also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the substracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10⁺ with electroporation method."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 606;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCCGAGGCGAGCTGGC 18
|||
Db 132 CCCGAGGCGAGCTGGC 115

RESULT 22
CB138393/c 612 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST0191254 L15CKK1 Homo sapiens cDNA clone L15CKK1-29-B07 5',
DEFINITION mRNA sequence.
ACCESSION CB138393
VERSION CB138393.1 GI:28110037
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 612)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001

TITLE Unpublished (2002)
JOURNAL
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boseun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 29 row: B column: 07
High quality sequence stop: 612.
Location/Qualifiers
1. 612

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L15CKK1-29-B07"
/sex="M"
/cell_line="CK-K1"
/lab_host="Top10⁺"
/clone_lib="L15CKK1"
/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI, Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10[®] by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 612;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCAGTCTGGC 18
DB 137 CCGGAGGAGCAGTCTGGC 120

RESULT 23 BE613913 622 bp mRNA linear EST 20-OCT-2000
LOCUS BE613913/c 601504033f1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905577 5',
DEFINITION mRNA sequence.

ACCESSION BE613913
VERSION BE613913.1 GI:3895510
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 622)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE Unpublished (1999)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

Plate: LMA9713 row: b column: 10
High quality sequence stop: 610.

FEATURES

source

Location/Qualifiers

1..622
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3905577"
/issue_type="telomysarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 71"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: Noti;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."

ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 622;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCAGTCTGGC 18
DB 96 CCGGAGGAGCAGTCTGGC 79

RESULT 24 AU131823 633 bp mRNA linear EST 01-AUG-2002
LOCUS AU131823/c

DEFINITION AU131823 NT2RP3 Homo sapiens cDNA clone NT2RP3003309 5', mRNA sequence.

ACCESSION AU131823
VERSION AU131823.1 GI:10992177

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 633)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saio, K., Kawai, Y., Yamamoto, J., Makatsutsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isega, T.

TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isega
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

Location/Qualifiers

1..633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP3003309"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_1ib="NT2RP3"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 633;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCAGTCTGGC 18
DB 130 CCGGAGGAGCAGTCTGGC 113

RESULT 25

CB134750 649 bp mRNA linear EST 29-JAN-2003

LOCUS K-EST186263 LSHLKI Homo sapiens cDNA clone LSHLKI-31-F08 5', mRNA sequence.

DEFINITION CB134750
ACCESSION CB134750
VERSION CB134750.1 GI:28101108

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 649)
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.krribb.re.kr

Plate: 31 row: F column: 08
High quality sequence stop: 649.
Location/Qualifiers

FEATURES

SOURCE

1. 649
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LSHLK1-31-P08"
/sex="M"
/cell_line="HLK-1"
/lab_host="Top10F"
/clone_1lb="LSHLK1"

/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tobacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transforation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 649;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 CCCGAAGGCGAGTCTGGC 18
DB 134 CCCGAAGGCGAGTCTGGC 117

RESULT 26

BG390105/c

LOCUS 602415946F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4524419 5',
DEFINITION mRNA sequence.

ACCESSION BG390105

VERSION BG390105.1 GI:13283651

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 657)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>

Plate: LLM10428 row: k column: 12
High quality sequence stop: 652.
Location/Qualifiers

FEATURES

SOURCE

1. 657
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4524419"
/tissue_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 2.5 Kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 657;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 CCCGAAGGCGAGTCTGGC 18
DB 119 CCCGAAGGCGAGTCTGGC 102

RESULT 27

B1832654/c

LOCUS 603082033F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5221137 5',
DEFINITION mRNA sequence.

ACCESSION B1832654

VERSION B1832654.1 GI:15944204

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 682)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>

Plate: LLM11556 row: a column: 10
High quality sequence stop: 680.
Location/Qualifiers

FEATURES

SOURCE

1. 682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5221137"
/lab_host="DH10B"

/clone_1lb="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 Kb, insert size range 1-2.5 Kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 682;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 CCCGAAGGCGAGTCTGGC 18
DB 105 CCCGAAGGCGAGTCTGGC 88

RESULT 28
AU121050/c
LOCUS AU121050
DEFINITION AU121050 Homo sapiens cDNA clone HEMBI001969 5', mRNA
sequence.
ACCESSION AU121050
VERSION AU121050.1 GI:10936285
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 688)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saico,K., Yamamoto,J.,
Yamamoto,T., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source
1..688
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBI001969"
/tissue_type="whole embryo, mainly body"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBI"
/note="Vector: pME18SF13"

ORIGIN
Query Match 100.0%; Score 18; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGGAGGCGACTGTGCG 18
DB 131 CCGGAGGCGACTGTGCG 114

RESULT 29
AU124510/c
LOCUS AU124510
DEFINITION AU124510 Homo sapiens cDNA clone NT2RM4000122 5', mRNA
sequence.
ACCESSION AU124510
VERSION AU124510.1 GI:10949226
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 694)
Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saico,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saico,K., Yamamoto,T., Nakamura,Y., Nishikawa,T., Nagai,T.,
Suzuki,Y., Sugano,S., Isogai,T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source
1..694
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM4000122"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RM4"
/note="Vector: pME18SF13; mRNA from uninduced NT2 neuronal
precursor cells"

ORIGIN
Query Match 100.0%; Score 18; DB 9; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGGAGGCGACTGTGCG 18
DB 133 CCGGAGGCGACTGTGCG 116

RESULT 30
BM011389/c
LOCUS BM011389
DEFINITION 603635585F1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5457909 5',
mRNA sequence.
ACCESSION BM011389
VERSION BM011389.1 GI:16525743
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 707)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgs@ds-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L10M1958 row: j column: 22
High quality sequence stop: 696.
Location/Qualifiers
1..707
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5457909"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 47"
/note="Organ. Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCAAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit

ORIGIN (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

Query Match 100.0%; Score 18; DB 12; Length 707;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
|||||
Db 118 CCCGAGAGCAGTCTGGC 101

RESULT 31
LOCUS AU141723 723 bp mRNA linear EST 05-AUG-2002
DEFINITION AU141723 THYR01 Homo sapiens cDNA clone THYR01001106 5', mRNA
sequence.
ACCESSION AU141723 GI:11003244
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 723)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Makamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1..723

FEATURES
source
1..723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="THYR01001106"
/tissue_type="thyroid gland"
/clone_lib="THYR01"
/note="Vector: pME18SFL3"

ORIGIN
Query Match 100.0%; Score 18; DB 9; Length 723;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
|||||
Db 137 CCCGAGAGCAGTCTGGC 120

RESULT 32
LOCUS AU131952 724 bp mRNA linear EST 01-AUG-2002
DEFINITION AU131952 NT2RP3 Homo sapiens cDNA clone NT2RP3003525 5', mRNA
sequence.
ACCESSION AU131952
VERSION AU131952.1 GI:10992306
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 724)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Makamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1..724

FEATURES
source
1..724
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP3003525"
/cell_type="keratinocarcinoma"
/cell_line="HT2"
/clone_lib="NT2RP3"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN
Query Match 100.0%; Score 18; DB 9; Length 724;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
|||||
Db 132 CCCGAGAGCAGTCTGGC 115

RESULT 33
LOCUS BM012402 726 bp mRNA linear EST 30-OCT-2001
DEFINITION 603636972F1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5459560 5',
mRNA sequence.
ACCESSION BM012402
VERSION BM012402.1 GI:16526756
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 726)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: InCyte Genomics, Inc.
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1962 row: o column: 17
High quality sequence stop: 542.
Location/Qualifiers
1..726
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5459560"

FEATURES
source
1..726
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5459560"

/tissue_type="neuroblastoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_47"
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI, Site 2:
 EcoRI; CDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 726;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAAAGGCACTCTGGC 18
 |||||
 123 CCCGAAAGGCACTCTGGC 106

RESULT 34
 AUI41300/c AUI41300 729 bp mRNA linear EST 05-ANG-2002
 LOCUS AUI41300 THYR01 Homo sapiens CDNA clone THYR01000362 5', mRNA
 DEFINITION sequence.
 ACCESSION AUI41300
 VERSION AUI41300.1 GI:11002821
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 729)
 Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, U., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
 Iwagaki, T.

TITLE HRI human CDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Iwagaki
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; CDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

Location/Qualifiers
 1..729

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="THYR01000362"
 /tissue_type="thyroid gland"
 /clone_lib="THYR01"
 /note="Vector: pME18SFL3"

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 729;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAAAGGCACTCTGGC 18
 |||||
 Db 132 CCCGAAAGGCACTCTGGC 115

RESULT 35

BM048582/c 732 bp mRNA linear EST 07-NOV-2001
 LOCUS BM048582
 DEFINITION 601623927F1 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:5449735 5',
 mRNA sequence.
 ACCESSION BM048582
 VERSION BM048582.1 GI:16777849
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 732)
 NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
 Plate: L10M1937 row: f column: 08
 High quality sequence stop: 715.
 Location/Qualifiers
 1..732

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5449735"
 /tissue_type="carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_40"
 /note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; CDNA made by oligo-dt priming;
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 732;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAAAGGCACTCTGGC 18
 |||||
 Db 120 CCCGAAAGGCACTCTGGC 103

RESULT 36

BE273022/c 744 bp mRNA linear EST 13-JUL-2000
 LOCUS BE273022
 DEFINITION 601171343F1 NIH_MGC_14 Homo sapiens CDNA clone IMAGE:5544714 5',
 mRNA sequence.
 ACCESSION BE273022
 VERSION BE273022.1 GI:9147377
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 744)
 NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov
Plate: L10CM240 row: f column: 11
High quality sequence stop: 639.

FEATURES

SOURCE

Location/Qualifiers
1..744
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3544714"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_14"
/note="Organ: Kidney; Vector: pOTB7, Site_1: XhoI, Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 744;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCGGAAGGAGCTGTGAC 18
|||||
Db 93 CCCGGAAGGAGCTGTGAC 76

RESULT 37
BM048815/c 750 bp mRNA linear EST 07-NOV-2001
LOCUS 603628360F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5456703 5',
DEFINITION mRNA sequence.
ACCESSION BM048815
VERSION BM048815.1 GI:16778082
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 750)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov
Plate: L10CM955 row: h column: 16
High quality sequence stop: 715.
Location/Qualifiers

FEATURES

SOURCE

1..750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5456703"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7, Site_1: XhoI, Site_2: EcoRI; cDNA made by oligo-dT priming."

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 750;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCGGAAGGAGCTGTGAC 18
|||||
Db 120 CCCGGAAGGAGCTGTGAC 103

RESULT 38
B1839050/c 758 bp mRNA linear EST 04-OCT-2001
LOCUS 603083048F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222266 5',
DEFINITION mRNA sequence.
ACCESSION B1839050
VERSION B1839050.1 GI:15950600
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 758)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov
Plate: L10M1558 row: p column: 11
High quality sequence start: 42
High quality sequence stop: 519.
Location/Qualifiers

FEATURES

SOURCE

1..758
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5222266"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRI (destroyed), RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 758;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCGGAAGGAGCTGTGAC 18
|||||
Db 146 CCCGGAAGGAGCTGTGAC 129

[illegible]

```

FEATURES
  source
    1..765
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:5452758"
      /tissue_type="carcinoma, cell line"
      /lab_host="DH108 (phage-resistant)"
      /note="Organ: prostate; Vector: pOTB7, Site 1: XhoI; Site 2: EcoRI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN
Query Match          100.0%; Score 18; DB 12; Length 765;
Best Local Similarity 100.0%; Pred. No.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dn      120 CCCGAGAGCAGCTGGC 103
      |||||
      1 CCCGAGAGCAGCTGGC 18

RESULT 41
BM046401/c          765 bp      mRNA      linear      EST 07-NOV-2001
LOCUS               603626426r1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5452758 5',
DEFINITION          mRNA sequence.
ACCESSION            BM046401
VERSION              BM046401.1 GI:16775668
KEYWORDS
SOURCE              Homo sapiens (human)
ORGANISM
  source
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
    1 (bases 1 to 765)
    NIH-MGC http://mgs.nci.nih.gov/
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strauberg, Ph. D.
    Email: cgapbs-remail.nih.gov
    Tissue Procurement: DCTD/DTF
    CDNA Library Preparation: Ling Hong/Rubin Laboratory
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LNLN at:
    http://image.lnl.gov
    Plate: L16CM1945 row: d column: 07
    High quality sequence stop: 544.
    Location/Qualifiers
      1..765
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:5452758"
        /tissue_type="carcinoma, cell line"
        /lab_host="DH108 (phage-resistant)"
        /clone_id="NIH_MGC_40"
        /note="Organ: prostate; Vector: pOTB7, Site 1: XhoI;
        Site 2: EcoRI, cDNA made by oligo-dT priming.

```


Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley), using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 765;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGAGAGGACAGTCTGGC 18
Db 120 CCCGAGAGGACAGTCTGGC 103

RESULT 42

BM048326 765 bp mRNA linear EST 07-NOV-2001
LOCUS 603625546F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5452187 5',
DEFINITION mRNA sequence.

ACCESSION BM048326
KEYWORDS EST,
SOURCE Homo sapiens (human)

REFERENCE 1 (bases 1 to 765)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCML943 row: 1 column: 12
High quality sequence stop: 341.
Location/Qualifiers

FEATURES

1..765
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5452187"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 765;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGAGAGGACAGTCTGGC 18
Db 115 CCCGAGAGGACAGTCTGGC 98

RESULT 43

BG481823/c 767 bp mRNA linear EST 21-MAR-2001
LOCUS 602529221F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4652690 5',
DEFINITION mRNA sequence.

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 767;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGAGAGGACAGTCTGGC 18
Db 110 CCCGAGAGGACAGTCTGGC 93

RESULT 44

AU120569 781 bp mRNA linear EST 01-AUG-2002
LOCUS AU120569 HENB1 Homo sapiens cDNA clone HENB100956 5', mRNA
DEFINITION sequence.

ACCESSION AU120569
KEYWORDS EST,
SOURCE Homo sapiens (human)

REFERENCE 1 (bases 1 to 781)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isegai, T.
JOURNAL HRI human cDNA project
COMMENT Unpublished (2000)
Contact: Takao Isegai

FEATURES

1..767
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4652690"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 767;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGAGAGGACAGTCTGGC 18
Db 110 CCCGAGAGGACAGTCTGGC 93

RESULT 45

Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES
 source

1..781
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HEMBA1000956"
 /tissue_type="whole embryo, mainly body"
 /dev_stage="embryo, 10 weeks"
 /clone_id="HEMBA1"
 /note="Vector: pME18SFL3"

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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCGGAAGGCGAGTCTGGC 18
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 Db 133 CCCGGAAGGCGAGTCTGGC 116

RESULT 45
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 LOCUS BI821174/c
 DEFINITION 6030350731 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175858 5',
 mRNA sequence.

ACCESSION BI821174
 VERSION BI821174.1 GI:15932724
 KEYWORDS EST.

SOURCE
 ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 808)
 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINT at:
 http://image.lnl.gov
 Plate: LHAM1438 row: b column: 19
 High quality sequence stop: 802.

FEATURES
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 /db_xref="taxon:9606"
 /clone="IMAGE:5175858"
 /lab_host="DH108"

/clone_id="NIH_MGC_115"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 808;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCGGAAGGCGAGTCTGGC 18
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 Db 104 CCCGGAAGGCGAGTCTGGC 87

RESULT 46
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 LOCUS BI905893/c
 DEFINITION 603063028F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212086 5',
 mRNA sequence.

ACCESSION BI905893
 VERSION BI905893.1 GI:16168494
 KEYWORDS EST.

SOURCE
 ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 815)
 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINT at:
 http://image.lnl.gov
 Plate: LHAM1532 row: h column: 07
 High quality sequence stop: 778.

FEATURES
 source

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 /db_xref="taxon:9606"
 /clone="IMAGE:5212086"
 /tissue_type="leukocyte"
 /lab_host="DH108"

/clone_id="NIH_MGC_118"
 /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 815;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 116 CCCGGAAGGCGAGTCTGGC 99

RESULT 47
 BU902747/c 817 bp mRNA linear EST 17-OCT-2002
 LOCUS BU902747

enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2004, 00:34:26 ; Search time 270 Seconds
(without alignments)
243.829 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18
Sequence: 1 cccgaagagcagctcggc 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2421054 seqs, 1828716029 residues

Total number of hits satisfying chosen parameters: 4842108

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database:

Published Applications NA.*
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	18	100.0	1303	15	US-10-397-635-6
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6	18	100.0	1317	10	US-09-829-922-1
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8	18	100.0	1760	10	US-09-849-602-9
9	18	100.0	1760	15	US-10-191-121-4
10	18	100.0	2209	15	US-10-063-674-2065
11	18	100.0	2521	15	US-10-428-802-25
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13	18	100.0	2629	12	US-10-391-068-1
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C 19	18	100.0	2629	15	US-10-165-216-3	Sequence 3, Appl
C 20	18	100.0	2629	15	US-10-159-563-188	Sequence 188, Appl
C 21	16.4	91.1	436	10	US-09-918-995-36880	Sequence 36880, Appl
C 22	16.4	91.1	905	14	US-10-066-543-113	Sequence 113, Appl
C 23	16.4	91.1	942	9	US-09-764-847-1845	Sequence 1845, Appl
C 24	16.4	91.1	942	9	US-09-764-847-1846	Sequence 1846, Appl
C 25	16.4	91.1	942	14	US-10-092-154-1845	Sequence 1845, Appl
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C 31	15.4	85.6	184	14	US-10-198-053-332	Sequence 332, Appl
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C 34	15.4	85.6	371	12	US-10-085-783A-21425	Sequence 21425, Appl
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C 46	15.4	85.6	405	13	US-10-025-180-755	Sequence 755, Appl
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C 190 13.8 76.7 304 15 US-10-242-535A-11602
C 191 13.8 76.7 345 9 US-09-867-701-5764
C 192 13.8 76.7 346 10 US-09-960-352-5306
C 193 13.8 76.7 347 9 US-09-764-891-1211
C 194 13.8 76.7 356 9 US-09-864-761-4069
C 195 13.8 76.7 372 10 US-09-918-995-30166
C 196 13.8 76.7 380 9 US-09-834-976-736
C 197 13.8 76.7 385 14 US-10-160-232-49
C 198 13.8 76.7 392 10 US-09-918-995-35200
C 199 13.8 76.7 396 9 US-09-796-692-3571
C 200 13.8 76.7 396 14 US-10-040-862-3571

ALIGNMENTS

US-09-848-868-35
Sequence 35, Application US/09848868
Publication No. US2003016568A1
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick L.
APPLICANT: Hudziak, Robert
TITLE OF INVENTION: Splice-Region Antisense Composition and
METHOD OF INVENTION: Splice-Region Antisense Composition and
FILE REFERENCE: 0450-0037.30
CURRENT APPLICATION NUMBER: US/09/848, 868
CURRENT FILING DATE: 2003-05-04
PRIORITY APPLICATION NUMBER: US 60/202,376
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense
US-09-848-868-35
Query Match 100.0% Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C 1 CCGGAGAGCGAGCTGCGC 18

Db 1 CCCGAGGAGCTGAC 18

RESULT 2

US-09-848-868-36
Sequence 36, Application US/09848868
Publication No. US20030166588A1
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick L.
APPLICANT: Hutzl, Robert
TITLE OF INVENTION: Splice-region Antisense Composition and
TITLE OF INVENTION: Method
FILE REFERENCE: 0450-0037.30
CURRENT APPLICATION NUMBER: US/09/848,868
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/202,376
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense
US-09-848-868-36

Query Match 100.0%; Score 18; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 CCCGAGGAGCTGAC 18
Db 17 CCCGAGGAGCTGAC 34

RESULT 3

US-09-776-695-22/c
Sequence 22, Application US/09776695
Patent No. US20020068283A1
GENERAL INFORMATION:

APPLICANT: Boeke, Jef
APPLICANT: Brachmann, Rainer
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
MUTATIONS WHICH SUPPRESS P53 CANCER MUTA- TIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,695
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,006
FILING DATE: 2001-03-28

ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299

TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-776-695-22

Query Match 100.0%; Score 18; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTGAC 18
Db 35 CCCGAGGAGCTGAC 18

RESULT 4

US-10-397-635-6/c
Sequence 6, Application US/10397635
Publication No. US2004009604A1
GENERAL INFORMATION:
APPLICANT: ZHANG, XIAOLI
APPLICANT: FU, XUPING
TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER
TITLE OF INVENTION: THERAPY
FILE REFERENCE: P0241082
CURRENT APPLICATION NUMBER: US/10/397,635
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/367,788
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/410,024
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 1303
TYPE: DNA
ORGANISM: Homo sapiens
US-10-397-635-6

Query Match 100.0%; Score 18; DB 15; Length 1303;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTGAC 18
Db 113 CCCGAGGAGCTGAC 96

RESULT 5

US-09-732-384-8/c
Sequence 8, Application US/09732384
Patent No. US20020132977A1
GENERAL INFORMATION:
APPLICANT: Yuan, Zhi-Min
APPLICANT: Gu, Jijie
TITLE OF INVENTION: Inhibition of p53 Degradation
FILE REFERENCE: 21508-044
CURRENT APPLICATION NUMBER: US/09/732,384
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/169,816
PRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 1307
TYPE: DNA
ORGANISM: Homo sapiens
US-09-732-384-8

Query Match 100.0%; Score 18; DB 9; Length 1307;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCTGGC 18
DB 117 CCGGAGGAGCTGGC 100

RESULT 6

US-09-829-922-1/c
; Sequence 1, Application US/09829922
; Publication No. US20030171537A1
; GENERAL INFORMATION:
; APPLICANT: Halazoneis, Thanos
; TITLE OF INVENTION: Peptides and peptidomimetics with
; TITLE OF INVENTION: structural similarity to human p53 that activate p53
; FILE REFERENCE: 2973.19998
; CURRENT APPLICATION NUMBER: US/09/829,922
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 08/894,327
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: pctus96/01535
; PRIOR FILING DATE: 1996-02-16
; PRIOR APPLICATION NUMBER: 08/392,542
; PRIOR FILING DATE: 1995-02-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-829-922-1

Query Match 100.0%; Score 18; DB 10; Length 1317;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCTGGC 18
DB 127 CCGGAGGAGCTGGC 110

RESULT 7

US-10-160-290-1/c
; Sequence 1, Application US/10160290
; Publication No. US20030124557A1
; GENERAL INFORMATION:
; APPLICANT: Halazoneis, Thanos
; TITLE OF INVENTION: Peptides and peptidomimetics with
; TITLE OF INVENTION: Structural Similarity to Human p53 That Activate
; p53
; FUNCTION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/160,290
; FILING DATE: 04-Jun-2002
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/685,027
FILING DATE: 10-Oct-2000
APPLICATION NUMBER: 08/392,542
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486,4839
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-160-290-1

Query Match 100.0%; Score 18; DB 14; Length 1317;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCTGGC 18
DB 127 CCGGAGGAGCTGGC 110

RESULT 8

US-09-849-602-9/c
; Sequence 9, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: U0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-849-602-9

Query Match 100.0%; Score 18; DB 10; Length 1760;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCTGGC 18
DB 206 CCGGAGGAGCTGGC 189

RESULT 9

US-10-191-121-4/c
; Sequence 4, Application US/10191121
; Publication No. US20040005574A1
; GENERAL INFORMATION:
; APPLICANT: Guarente, Leonard
; APPLICANT: Vaziri, Homayoun
; APPLICANT: Imai, Shin-Ichiro
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: Sir2 and p53 Deacetylation

```
FILE REFERENCE: 13407-015002
CURRENT APPLICATION NUMBER: US/10/191,121
CURRENT FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: US 60/303,456
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 10/NNN,NNN
PRIOR FILING DATE: 2002-07-05
PRIOR APPLICATION NUMBER: US 60/303,370
PRIOR FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 1760
TYPE: DNA
ORGANISM: Homo sapiens
US-10-191-121-4

Query Match
Best Local Similarity 100.0%; Score 18; DB 15; Length 1760;
Pred. No. 7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCGGAAGGCGAGTCTGGC 18
Db 206 CCCGGAAGGCGAGTCTGGC 189

RESULT 10
US-10-062-674-2065/c
Sequence 2065, Application US/10062674
Publication No. US20040005559A1
GENERAL INFORMATION:
APPLICANT: Loiring, Jeanne F.; Kaser, Matthew R.
TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
FILE REFERENCE: PA-0026-1 CIP
CURRENT APPLICATION NUMBER: US/10/062,674
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: US 09/625,102
PRIOR FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 2217
SOFTWARE: PERL Program
SEQ ID NO 2065
LENGTH: 2209
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incycle ID No. US20040005559A1 430224.2
US-10-062-674-2065

Query Match
Best Local Similarity 100.0%; Score 18; DB 15; Length 2209;
Pred. No. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCGGAAGGCGAGTCTGGC 18
Db 170 CCCGGAAGGCGAGTCTGGC 153

RESULT 11
US-10-429-802-25/c
Sequence 25, Application US/10429802
Publication No. US20030228285A1
GENERAL INFORMATION:
APPLICANT: HUNG, MIEN-CHIE
APPLICANT: ZOU, YIYU
TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
FILE REFERENCE: UTSC:752US
CURRENT APPLICATION NUMBER: US/10/429,802
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: 60/377,672
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 54
```

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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 2521
TYPE: DNA
ORGANISM: Homo sapiens
US-10-429-802-25

Query Match
Best Local Similarity 100.0%; Score 18; DB 15; Length 2521;
Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCGGAAGGCGAGTCTGGC 18
Db 127 CCCGGAAGGCGAGTCTGGC 110

RESULT 12
US-10-430-503-16/c
Sequence 16, Application US/10430503
Publication No. US20040005684A1
GENERAL INFORMATION:
APPLICANT: HUNG, MIEN-CHIE
APPLICANT: LAN, KENG-LI
APPLICANT: OU-YANG, FU
APPLICANT: LIU, JAW-CHING
APPLICANT: LAN, KENG-HSIN
TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
FILE REFERENCE: UTSC:797US
CURRENT APPLICATION NUMBER: US/10/430,503
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/383,063
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 2521
TYPE: DNA
ORGANISM: Homo sapiens
US-10-430-503-16

Query Match
Best Local Similarity 100.0%; Score 18; DB 15; Length 2521;
Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCGGAAGGCGAGTCTGGC 18
Db 127 CCCGGAAGGCGAGTCTGGC 110

RESULT 13
US-10-391-068-1/c
Sequence 1, Application US/10391068
Publication No. US20040028654A1
GENERAL INFORMATION:
APPLICANT: UT, LIN
APPLICANT: ROTH, JACK
TITLE OF INVENTION: PROTAINE-ADENOVIRAL VECTOR COMPLEXES
FILE REFERENCE: INRP:097US
CURRENT APPLICATION NUMBER: US/10/391,068
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: 60/366,846
PRIOR FILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2625
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (252)...(1433)
```

US-10-391-068-1

Query Match 100.0%; Score 18; DB 12; Length 2625;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 14
US-10-077-176-58/c
; Sequence 58, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008
; CURRENT APPLICATION NUMBER: US/10/077,176
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-176-58

Query Match 100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 15
US-10-077-176-59/c
; Sequence 59, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008
; CURRENT APPLICATION NUMBER: US/10/077,176
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-176-59

Query Match 100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 16
US-10-077-176-60/c
; Sequence 60, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008

CURRENT APPLICATION NUMBER: US/10/077,176
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-176-60

Query Match 100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 17
US-10-077-176-61/c
; Sequence 61, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008
; CURRENT APPLICATION NUMBER: US/10/077,176
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-176-61

Query Match 100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 18
US-10-439-388-16/c
; Sequence 16, Application US/10439388
; Publication No. US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M
; APPLICANT: Olsen, Nancy J
; TITLE OF INVENTION: Method for Predicting Autoimmune Disease
; FILE REFERENCE: 1242/68
; CURRENT APPLICATION NUMBER: US/10/439,388
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,055
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-439-388-16

Query Match 100.0%; Score 18; DB 15; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||

Db 243 CCCGAGGAGCTCTGGC 226

RESULT 19
US-10-165-216-3/c
; Sequence 3, Application US/10165216
; Publication No. US20030228675A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Diane M.
; APPLICANT: Abraham, Robert T.
; TITLE OF INVENTION: ATM Related Kinase ATX, Nucleic Acids
; FILE REFERENCE: P-LJ 5222
; CURRENT APPLICATION NUMBER: US/10/165,216
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (252)... (1433)
US-10-165-216-3

Query Match 100.0%; Score 18; DB 15; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTCTGGC 18
Db 243 CCCGAGGAGCTCTGGC 226

RESULT 20
US-10-159-563-188/c
; Sequence 188, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TREATING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613, 56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-188

Query Match 100.0%; Score 18; DB 15; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTCTGGC 18
Db 243 CCCGAGGAGCTCTGGC 226

RESULT 21
US-09-918-995-36880/c
; Sequence 36880, Application US/09918995
; Publication No. US2003007363A1
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36880
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-36880

Query Match 91.1%; Score 16.4; DB 10; Length 436;
Best Local Similarity 94.4%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTCTGGC 18
Db 90 CCCGAGGAGCTCTGGC 73

RESULT 22
US-10-066-543-113/c
; Sequence 113, Application US/10066543
; Publication No. US2003008781B1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indira, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margareta
; APPLICANT: Stoik, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 13, 45, 386, 545, 580, 582, 584, 590, 591, 603, 606, 609,
; LOCATION: 610, 616, 621, 623, 624, 625, 629, 630, 646, 652, 670, 672,
; LOCATION: 674, 676, 688, 700, 709, 710, 744, 753, 756, 758, 763,
; LOCATION: 786, 796, 823, 851, 876, 885
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-113

Query Match 91.1%; Score 16.4; DB 14; Length 905;
Best Local Similarity 94.4%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTCTGGC 18
Db 516 CCCGAGGAGCTCTGGC 499

RESULT 23
US-09-764-847-1845/c
; Sequence 1845, Application US/09764847

```

; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1845
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-847-1845

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 9; Length 942;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
Db 58 CCCGGAAGGCGAGTCTGTC 41

RESULT 24
; US-09-764-847-1846/c
; Sequence 1846, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1846
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-847-1846

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 9; Length 942;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
Db 58 CCCGGAAGGCGAGTCTGTC 41

RESULT 25
; US-10-092-154-1845/c
; Sequence 1845, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009c1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior application removed - See file wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1845
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-092-154-1845

Query Match
91.1%; Score 16.4; DB 14; Length 942;
Score 16.4; DB 14; Length 942;

QY 1 CCCGGAAGGCGAGTCTGGC 18
Db 58 CCCGGAAGGCGAGTCTGTC 41

RESULT 26
; US-10-092-154-1846/c
; Sequence 1846, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009c1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior application removed - See file wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1846
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-092-154-1846

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 14; Length 942;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
Db 58 CCCGGAAGGCGAGTCTGTC 41

RESULT 27
; US-09-765-231A-2/c
; Sequence 2, Application US/09765231A
; Patent No. US20020119452A1
; GENERAL INFORMATION:
; APPLICANT: Searle/Monsanto
; APPLICANT: Philipard, Deborah
; APPLICANT: Vasanthakumari, Geetha
; APPLICANT: Dotson, Stanton
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
; TITLE OF INVENTION: vectors, and cells
; FILE REFERENCE: SO-3221 PR
; CURRENT APPLICATION NUMBER: US/09/765,231A
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 82
; SEQ ID NO 2
; LENGTH: 1986
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-765-231A-2

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 9; Length 1986;
Best Local Similarity 94.4%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
Db 893 CCCGGAAGGCGAGTCTGGC 876

RESULT 28
; US-09-884-441-332
; Sequence 332, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
```

```

; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-441-332

Query Match      85.6%; Score 15.4; DB 9; Length 184;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CCGAAGGCGAGTCTGGC 18
Db      112 CCAGAAGGCGAGTCTGGC 128

RESULT 29
US-09-907-969-332
; Sequence 332, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-969-332

Query Match      85.6%; Score 15.4; DB 10; Length 184;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CCGAAGGCGAGTCTGGC 18
Db      112 CCAGAAGGCGAGTCTGGC 128

RESULT 30
US-09-827-271-332
; Sequence 332, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
```

```

; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-271-332

Query Match      85.6%; Score 15.4; DB 10; Length 184;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CCGAAGGCGAGTCTGGC 18
Db      112 CCAGAAGGCGAGTCTGGC 128

RESULT 31
US-10-198-053-332
; Sequence 332, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-053-332

Query Match      85.6%; Score 15.4; DB 14; Length 184;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CCGAAGGCGAGTCTGGC 18
Db      112 CCAGAAGGCGAGTCTGGC 128

RESULT 32
US-10-085-783A-47890/C
; Sequence 47890, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47890
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-47890
```

Query Match 85.6%; Score 15.4; DB 12; Length 358;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 358 CCGAAGGCACTCTGGC 342

RESULT 33
US-10-242-535A-47890/c
Sequence 47890, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 47890
LENGTH: 358
TYPE: DNA
ORGANISM: Human
US-10-242-535A-47890

Query Match 85.6%; Score 15.4; DB 15; Length 358;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 358 CCGAAGGCACTCTGGC 342

RESULT 34
US-10-085-783A-21425/c
Sequence 21425, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21425
LENGTH: 371
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:

NAME/KEY: misc_feature
LOCATION: (203)..(203)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (205)..(206)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-21425

Query Match 85.6%; Score 15.4; DB 12; Length 371;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 165 CCGAAGGCACTCTGGC 149

RESULT 35
US-10-242-535A-21425/c
Sequence 21425, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21425
LENGTH: 371
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (203)..(203)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (205)..(206)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-21425

Query Match 85.6%; Score 15.4; DB 15; Length 371;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 165 CCGAAGGCACTCTGGC 149

RESULT 36
US-10-085-783A-9459/c
Sequence 9459, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.


```

; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23153
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (56)..(56)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (67)..(68)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (212)..(212)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-242-535A-23153
```

```

Query Match      85.6%; Score 15.4; DB 15; Length 397;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CCGAAGGCACTCTGAC 18
DB      85 CCGAAGGCACTCTGAC 69
```

```

RESULT 40
; US-10-085-783A-23042/c
; Sequence 23042, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23042
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (42)..(42)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-085-783A-23042
```

```

Query Match      85.6%; Score 15.4; DB 12; Length 399;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CCGAAGGCACTCTGAC 18
DB      351 CCGAAGGCACTCTGAC 335
```

```

RESULT 41
; US-10-242-535A-23042/c
; Sequence 23042, Application US/10242535A
; Publication No. US20040013653A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23042
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (42)..(42)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-242-535A-23042
```

```

Query Match      85.6%; Score 15.4; DB 15; Length 399;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CCGAAGGCACTCTGAC 18
DB      351 CCGAAGGCACTCTGAC 335
```

```

RESULT 42
; US-10-085-783A-23133/c
; Sequence 23133, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23133
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (40)..(40)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: (48)..(48)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (341)..(341)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (394)..(394)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-23133

Query Match 85.6%; Score 15.4; DB 12; Length 400;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 36 CCGAAGGCACTCTGGC 20

RESULT 43
US-10-242-535A-23133/c
Sequence 23133, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: Chondrogene Inc.
APPLICANT: Liaw, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23133
LENGTH: 400.
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(7)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (40)..(40)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (48)..(48)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (341)..(341)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (394)..(394)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-23133

Query Match 85.6%; Score 15.4; DB 15; Length 400;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18

DB 36 CCGAAGGCACTCTGGC 20

RESULT 44
US-09-922-217-755/c
Sequence 755, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeline Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tonglong
APPLICANT: Jiang, Yudi
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aljun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 755
LENGTH: 405
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 214, 305, 366, 368, 378
OTHER INFORMATION: n = A,T,C or G
US-09-922-217-755

Query Match 85.6%; Score 15.4; DB 9; Length 405;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 213 CCGAAGGCACTCTGGC 197

RESULT 45
US-09-833-263-755/c
Sequence 755, Application US/09833263
Patent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aljun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeline J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 755
LENGTH: 405
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(405)
OTHER INFORMATION: n = A,T,C or G
US-09-833-263-755

Query Match 85.6%; Score 15.4; DB 9; Length 405;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTGGC 18
DB 213 CCGAAGGCACTGGC 197

RESULT 46
US-10-025-380-755/c

; Sequence 755, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedyck, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025.380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 755
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 214, 305, 366, 368, 378
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-755

Query Match 85.6%; Score 15.4; DB 13; Length 405;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTGGC 18
DB 213 CCGAAGGCACTGGC 197

RESULT 47
US-10-085-783A-58222/c

; Sequence 58222, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085.783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58222
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56)..(56)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-58222

Query Match 85.6%; Score 15.4; DB 12; Length 422;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTGGC 18
DB 305 CCGAAGGCACTGGC 289

RESULT 48
US-10-242-535A-58222/c

; Sequence 58222, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242.535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58222
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56)..(56)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-58222

Query Match 85.6%; Score 15.4; DB 15; Length 422;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTGGC 18
DB 305 CCGAAGGCACTGGC 289

RESULT 49
US-10-085-783A-17255/c

; Sequence 17255, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085.783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 23:56:01 ; Search time 80 Seconds
(without alignments)

124.864 Million cell updates/sec

Title: US-09-848-868-35
Perfect score: 18
Sequence: 1 cccggaagcagctctgc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 200 summaries

Database : Issued Patents_NA.*
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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	18	100.0	133	3	US-09-184-073-42
5	18	100.0	800	1	US-08-472-239-1
6	18	100.0	1070	3	US-09-414-436-4
7	18	100.0	1303	1	US-08-047-041A-13
8	18	100.0	1307	1	US-08-047-041A-12
9	18	100.0	1317	1	US-07-912-011-1
10	18	100.0	1317	1	US-08-347-792-1
11	18	100.0	1317	1	US-08-431-357-1
12	18	100.0	1317	2	US-08-697-321-1
13	18	100.0	1317	3	US-08-392-542-1
14	18	100.0	1317	3	US-08-894-337-1
15	18	100.0	1317	4	US-09-147-751-8
16	18	100.0	1317	4	US-09-305-924-1
17	18	100.0	1317	4	US-09-685-027-1
18	18	100.0	1317	5	PCT-US95-15153-1
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21	15.4	85.6	447	4	US-09-736-457-1634
22	15.4	85.6	447	4	US-09-614-124B-1634
23	15.4	85.6	447	4	US-08-671-325-1634
24	15.4	85.6	633	3	US-09-385-982-806
25	15.4	85.6	647	4	US-09-222-575-81
26	15.4	85.6	647	4	US-09-389-681-81
27	15.4	85.6	647	4	US-09-620-405B-81

28	15.4	85.6	647	4	US-09-339-338-81	Sequence 81, Appl
29	15.4	85.6	647	4	US-09-433-826B-81	Sequence 81, Appl
30	15.4	85.6	647	4	US-09-604-287A-81	Sequence 81, Appl
31	15.4	85.6	647	4	US-09-285-480-81	Sequence 81, Appl
32	15.4	85.6	647	4	US-09-834-759-81	Sequence 81, Appl
33	15	83.3	25	1	US-08-447-179-7	Sequence 7, Appl
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37	14.8	82.2	8078	3	US-08-870-126-12	Sequence 12, Appl
38	14.8	82.2	8078	4	US-09-445-247-12	Sequence 12, Appl
39	14.8	82.2	14985	1	US-08-652-972A-6	Sequence 6, Appl
40	14.8	82.2	14985	5	PCT-US96-06231A-6	Sequence 6, Appl
41	14.8	82.2	4403765	3	US-09-103-840A-2	Sequence 2, Appl
42	14.8	82.2	4411529	3	US-09-103-840A-1	Sequence 11048, A
43	14.4	80.0	252	4	US-09-621-976-11048	Sequence 3, Appl
44	14.4	80.0	360	1	US-08-256-077-3	Sequence 3, Appl
45	14.4	80.0	360	1	US-08-466-127-3	Sequence 1, Appl
46	14.4	80.0	982	1	US-08-256-077-1	Sequence 1, Appl
47	14.4	80.0	982	1	US-08-466-127-1	Sequence 1, Appl
48	14	77.8	8137	4	US-09-566-921-7	Sequence 1, Appl
49	13.8	76.7	157	3	US-08-721-986-1	Sequence 1, Appl
50	13.8	76.7	157	3	US-08-225-487A-1	Sequence 28, Appl
51	13.8	76.7	212	1	US-08-435-684A-28	Sequence 28, Appl
52	13.8	76.7	212	2	US-08-934-877A-28	Sequence 1, Appl
53	13.8	76.7	212	3	US-08-871-678C-28	Sequence 1, Appl
54	13.8	76.7	237	4	US-09-252-591A-10772	Sequence 2, Appl
55	13.8	76.7	371	4	US-08-885-593A-35	Sequence 188, Appl
56	13.8	76.7	441	4	US-08-914-795C-53	Sequence 188, Appl
57	13.8	76.7	579	4	US-09-404-879A-188	Sequence 188, Appl
58	13.8	76.7	579	4	US-09-338-933-188	Sequence 188, Appl
59	13.8	76.7	579	4	US-09-215-681-188	Sequence 188, Appl
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61	13.8	76.7	584	4	US-09-404-879A-187	Sequence 187, Appl
62	13.8	76.7	584	4	US-09-338-933-187	Sequence 187, Appl
63	13.8	76.7	584	4	US-09-215-681-187	Sequence 187, Appl
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67	13.8	76.7	655	4	US-09-643-597-208	Sequence 208, Appl
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73	13.8	76.7	771	4	US-09-328-352-3448	Sequence 3448, Appl
74	13.8	76.7	854	1	US-08-166-195A-1	Sequence 1, Appl
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76	13.8	76.7	854	1	US-08-336-772-1	Sequence 1, Appl
77	13.8	76.7	855	4	US-09-252-991A-10688	Sequence 10688, A
78	13.8	76.7	879	4	US-09-894-844-46	Sequence 46, Appl
79	13.8	76.7	987	4	US-09-252-991A-15247	Sequence 15247, A
80	13.8	76.7	993	4	US-09-833-381-895	Sequence 895, Appl
81	13.8	76.7	1001	4	US-09-671-317-230	Sequence 230, Appl
82	13.8	76.7	1001	4	US-09-671-317-231	Sequence 231, Appl
83	13.8	76.7	1032	4	US-09-016-434-1338	Sequence 1338, Appl
84	13.8	76.7	1176	4	US-09-252-991A-15444	Sequence 15444, A
85	13.8	76.7	1290	4	US-09-107-532A-3539	Sequence 3539, Appl
86	13.8	76.7	1344	4	US-09-252-991A-15551	Sequence 15551, A
87	13.8	76.7	1365	4	US-09-489-039A-493	Sequence 493, Appl
88	13.8	76.7	1392	4	US-09-252-991A-11115	Sequence 11115, A
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90	13.8	76.7	1403	3	US-08-751-344B-1	Sequence 1, Appl
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92	13.8	76.7	1410	3	US-09-255-366A-1	Sequence 1, Appl
93	13.8	76.7	1413	4	US-09-252-991A-11233	Sequence 11233, A
94	13.8	76.7	1416	4	US-09-252-991A-10948	Sequence 10948, A
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96	13.8	76.7	1474	2	US-09-053-303-1	Sequence 1, Appl
97	13.8	76.7	1474	2	US-09-339-115-1	Sequence 1, Appl
98	13.8	76.7	1474	5	PCT-US95-07093-1	Sequence 1, Appl
99	13.8	76.7	1613	4	US-09-061-154-1	Sequence 1, Appl
100	13.8	76.7	1613	4	US-09-061-154-3	Sequence 3, Appl

101 13.8 76.7 1614 1 US-08-583-672-1 Sequence 1, Applt
102 13.8 76.7 1640 1 US-07-796-361A-12 Sequence 12, Applt
103 13.8 76.7 1665 4 US-09-252-991A-10272 Sequence 10272, A
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105 13.8 76.7 1816 1 US-08-539-666-3 Sequence 3, Applt
106 13.8 76.7 1817 1 US-07-612-673-3 Sequence 3, Applt
107 13.8 76.7 1917 4 US-09-252-991A-8634 Sequence 8634, Ap
108 13.8 76.7 1924 4 US-09-533-499A-1 Sequence 1, Applt
109 13.8 76.7 2186 2 US-08-878-546-9 Sequence 9, Applt
110 13.8 76.7 2935 1 US-08-246-583-1 Sequence 1, Applt
111 13.8 76.7 2940 4 US-09-636-791A-3 Sequence 3, Applt
112 13.8 76.7 3475 3 US-09-657-481A-10 Sequence 10, Applt
113 13.8 76.7 3476 3 US-08-630-916A-17 Sequence 47, Applt
114 13.8 76.7 3519 1 US-08-285-889-45 Sequence 45, Applt
115 13.8 76.7 3519 1 US-08-485-618-45 Sequence 45, Applt
116 13.8 76.7 3519 1 US-08-362-652-45 Sequence 45, Applt
117 13.8 76.7 3519 1 US-08-605-672-45 Sequence 45, Applt
118 13.8 76.7 3519 2 US-08-482-293A-45 Sequence 45, Applt
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156 13.8 76.7 50341 2 US-09-075-904-1 Sequence 1, Applt
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168 13.4 74.4 288 4 US-09-252-991A-3404 Sequence 3404, Ap
169 13.4 74.4 417 4 US-09-216-393B-15 Sequence 15, Applt
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172 13.4 74.4 506 2 US-08-799-173A-15 Sequence 15, Applt
173 13.4 74.4 601 4 US-09-814-951A-11 Sequence 11, Applt

174 13.4 74.4 620 3 US-09-328-111-490 Sequence 490, App
175 13.4 74.4 783 4 US-09-023-655-28 Sequence 28, Applt
176 13.4 74.4 909 4 US-09-252-991A-3246 Sequence 3246, Ap
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178 13.4 74.4 1105 2 US-08-799-173A-1 Sequence 1, Applt
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182 13.4 74.4 1543 4 US-09-364-230-17 Sequence 17, Applt
183 13.4 74.4 1779 3 US-09-371-696-1 Sequence 1, Applt
184 13.4 74.4 1785 4 US-09-732-957B-1 Sequence 1, Applt
185 13.4 74.4 1885 4 US-09-484-970B-127 Sequence 127, App
186 13.4 74.4 1995 4 US-09-252-991A-3392 Sequence 3392, Ap
187 13.4 74.4 2156 1 US-08-178-477B-31 Sequence 31, Applt
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189 13.4 74.4 2156 4 US-09-023-655-1111 Sequence 1111, Ap
190 13.4 74.4 2912 3 US-09-034-177-2 Sequence 2, Applt
191 13.4 74.4 3539 3 US-08-853-948B-1 Sequence 1, Applt
192 13.4 74.4 4100 4 US-09-620-312D-1071 Sequence 1071, Ap
193 13.4 74.4 4768 1 US-07-586-467-1 Sequence 1, Applt
194 13.4 74.4 4768 1 US-07-934-374-1 Sequence 1, Applt
195 13.4 74.4 4768 1 US-07-783-661C-3 Sequence 3, Applt
196 13.4 74.4 11561 1 US-08-450-332-1 Sequence 1, Applt
197 13.4 74.4 11561 2 US-08-637-640-1 Sequence 1, Applt
198 13.4 74.4 11561 3 US-09-004-406C-1 Sequence 1, Applt
199 13.4 74.4 33000 4 US-09-215-694-18 Sequence 18, Applt
200 13.2 73.3 21 4 US-09-632-675-8 Sequence 8, Applt

RESULT 1
US-08-047-041A-15/C
Sequence 15, Application US/08047041A
Patent No. 5567676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of Loss of the wild-Type p53
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001.4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0107.42917

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: exon 2
PUBLICATION INFORMATION:
AUTHORS: Lamb,
JOURNAL: Mol. Cell. Biol.
VOLUME: 6
ISSUE: 5
PAGES: 1379-1385
DATE: 1986
US-08-047-041A-15

Query Match 100.0%; Score 18; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGCG 18
DB 20 CCGGAGGCGAGTCTGCG 3

RESULT 2
US-08-047-041A-2/c
Sequence 2, Application US/08047041A
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Pearson, Eric R.
TITLE OF INVENTION: Detection of loss of the wild-type p53
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allgretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001, 4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: exon 2
PUBLICATION INFORMATION:
AUTHORS: Buchman, V. L.
TITLE: A variation in the structure of the
TITLE: protein-coding region of the human p53 gene
JOURNAL: Gene
VOLUME: 70
PAGES: 245-252
DATE: 1986
US-08-047-041A-2

Query Match 100.0%; Score 18; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGCG 18
DB 35 CCGGAGGCGAGTCTGCG 18

RESULT 3
US-08-795-006A-22/c
Sequence 22, Application US/08795006A
GENERAL INFORMATION:
APPLICANT: Boeke, Jef
APPLICANT: Brachmann, Rainer
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
TITLE OF INVENTION: MUTATIONS WHICH SUPPRESS P53 CANCER MUTA- TIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wilcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,006A
FILING DATE: 05-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107,03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-795-006A-22

Query Match 100.0%; Score 18; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGCTGTGGC 18
DB 35 CCCGGAAGGCGAGCTGTGGC 18

RESULT 4
US-09-184-073-22/c
Sequence 22, Application US/09184073

PATENT No. 6183964
GENERAL INFORMATION:
APPLICANT: Boeke, Jef
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
TITLE OF INVENTION: MUTATIONS WHICH SUPPRESS P53 CANCER MUTA- TIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,073
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,006
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107,03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-184-073-22

Query Match 100.0%; Score 18; DB 3; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGCTGTGGC 18
DB 35 CCCGGAAGGCGAGCTGTGGC 18

RESULT 5
US-08-472-239-1/c
Sequence 1, Application US/08472239

PATENT No. 5728526
GENERAL INFORMATION:
APPLICANT: GEORGE, Jr., Albert L.
APPLICANT: BHATTNAGAR, Satish K.
APPLICANT: NAZARENKO, Irena
TITLE OF INVENTION: METHOD FOR ANALYZING A NUCLEOTIDE
TITLE OF INVENTION: SEQUENCE AND KIT THEREFOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATIIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,239
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mukai, Robert G.
REGISTRATION NUMBER: 28,531
REFERENCE/DOCKET NUMBER: 020160-229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-472-239-1

Query Match 100.0%; Score 18; DB 1; Length 800;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGCTGTGGC 18
DB 108 CCCGGAAGGCGAGCTGTGGC 91

RESULT 6
US-09-414-436-4/c
Sequence 4, Application US/09414436
PATENT No. 6294384
GENERAL INFORMATION:
APPLICANT: Dell'Acqua, Giorgio
APPLICANT: Mann, Michael J.
APPLICANT: Dzaou, Victor J.
TITLE OF INVENTION: Compositions and Methods Based Upon an Isoform of p53
FILE REFERENCE: p53f
CURRENT APPLICATION NUMBER: US/09/414,436
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: 60/103,849
EARLIER FILING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 4
LENGTH: 1070
TYPE: DNA
ORGANISM: Homo sapiens
US-09-414-436-4

Query Match 100.0%; Score 18; DB 3; Length 1070;
Best Local Similarity 100.0%; Pred. No. 4.3;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGAGGAGCTGAC 18
Db 127 CCGGAGGAGCTGAC 110

RESULT 7
US-08-047-041A-13/c
Sequence 13, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of loss of the wild-type p53
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001.4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
MAP POSITION: 17p13.1
PUBLICATION INFORMATION:
AUTHORS: Harris, N.
JOURNAL: Mol. Cell. Biol
VOLUME: 6
ISSUE: 12
PAGES: 4650-4656
DATE: 1986
US-08-047-041A-13

Query Match 100.0%; Score 18; DB 1; Length 1303;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGAGGAGCTGAC 18
Db 113 CCGGAGGAGCTGAC 96

RESULT 8
US-08-047-041A-12/c
Sequence 12, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of loss of the wild-type p53
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001.4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
MAP POSITION: 17p13.1
PUBLICATION INFORMATION:
AUTHORS: Harris, N.
TITLE: Molecular basis for heterogeneity of the
TITLE: human p53 protein
JOURNAL: Mol. Cell. Biol.
VOLUME: 6
ISSUE: 12

PAGES: 4650-4656
DATE: 1986
US-08-047-041A-12

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 1307;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGAGCTCTGGC 18
DB 117 CCCGGAAGGAGCTCTGGC 100

RESULT 9
US-07-912-011-1/C
Sequence 1, Application US/07912011
Patent No. 5382510
GENERAL INFORMATION:
APPLICANT: Levine, Arnold J.
APPLICANT: Shenk, Thomas E.
APPLICANT: Finlay, Cathy A.
TITLE OF INVENTION: Probes for Detecting Mutant p53
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912.011
FILING DATE: 10-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28, 601
REFERENCE/DOCKET NUMBER: LEV-1-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-912-011-1

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 1317;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGAGCTCTGGC 18
DB 127 CCCGGAAGGAGCTCTGGC 110

RESULT 10
US-08-347-792-1/C
Sequence 1, Application US/08347792
Patent No. 5573925
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thomas D.
TITLE OF INVENTION: p53 Proteins With Altered
Tetramerization Domains
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,792
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: MST58USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
US-08-347-792-1

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 1317;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGAGCTCTGGC 18
DB 127 CCCGGAAGGAGCTCTGGC 110

RESULT 11
US-08-431-357-1/C
Sequence 1, Application US/08431357
Patent No. 5721340
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thomas D.
TITLE OF INVENTION: p53 Proteins With Altered
Tetramerization Domains
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: W515805A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
US-08-431-357-1

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 1317;
Pred. No. 4.3; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 127 CCCGAGGCGAGTCTGGC 110

RESULT 12
US-08-697-221-1/c
Sequence 1, Application US/08697221
Patent No. 5847083
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: Modified p53 Constructs and Uses
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,221
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,802
FILING DATE: 22-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: W5164AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
US-08-697-221-1

Query Match
Best Local Similarity 100.0%; Score 18; DB 2; Length 1317;
Pred. No. 4.3; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 127 CCCGAGGCGAGTCTGGC 110

RESULT 13
US-08-392-542-1/c
Sequence 1, Application US/08392542
Patent No. 6169073
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
TITLE OF INVENTION: Peptides and peptidomimetics with
STRUCTURAL SIMILARITY TO HUMAN P53 THAT ACTIVATE P53
TITLE OF INVENTION: Function
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,542
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486.48439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9289
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-392-542-1

Query Match
Best Local Similarity 100.0%; Score 18; DB 3; Length 1317;
Pred. No. 4.3; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 127 CCCGAGGCGAGTCTGGC 110

RESULT 14
US-08-894-327-1/c
Sequence 1, Application US/08894327
Patent No. 6245886
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
TITLE OF INVENTION: Peptides and peptidomimetics with
STRUCTURAL SIMILARITY TO HUMAN P53 THAT ACTIVATE P53
TITLE OF INVENTION: structural similarity to human p53 that activate p53

TITLE OF INVENTION: function
FILE REFERENCE: 2973.1998
CURRENT APPLICATION NUMBER: US/08/894,327
CURRENT FILING DATE: 1997-12-04
EARLIER APPLICATION NUMBER: pctus96/01535
EARLIER FILING DATE: 1996-02-16
EARLIER APPLICATION NUMBER: 08/392,542
EARLIER FILING DATE: 1995-02-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1317
TYPE: DNA
ORGANISM: Homo sapiens
US-08-894-327-1

Query Match 100.0%; Score 18; DB 3; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTCTGGC 18
DB 127 CCCGGAAGCAGCTCTGGC 110

RESULT 15
US-09-147-751-8/c
Sequence 8, Application US/09147751
Patent No. 6335164
GENERAL INFORMATION:
APPLICANT: KIGAWA, Koji
APPLICANT: YAMANAKA, Mikayo
APPLICANT: KUSUMI, Kayo
APPLICANT: MUKAI, Eiji
APPLICANT: OBARA, Kazuaki
TITLE OF INVENTION: METHODS FOR TARGETING, ENRICHING,
TITLE OF INVENTION: DETECTING AND/OR ISOLATING TARGET NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: USING RECA-LIKE RECOMBINASE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/147,751
FILING DATE: 18-MAY-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP97/03019
FILING DATE: 23-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8/347090
FILING DATE: 26-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8/229061
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Maehius, Stephen B.
REGISTRATION NUMBER: 35,264
REFERENCE/DOCKET NUMBER: 84335/108
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-09-147-751-8

Query Match 100.0%; Score 18; DB 4; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTCTGGC 18
DB 127 CCCGGAAGCAGCTCTGGC 110

RESULT 16
US-09-305-914-1/c
Sequence 1, Application US/09305914
Patent No. 6388062
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos D.
APPLICANT: Stavridi, Elena S.
TITLE OF INVENTION: Modified p53 Tetramerization Domains Having Hydrophobic
TITLE OF INVENTION: Amino Acid Substitutions
FILE REFERENCE: W8784AUSA
CURRENT APPLICATION NUMBER: US/09/305,914
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: 60/084,839
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1317
TYPE: DNA
ORGANISM: human p53
FEATURE:
NAME/KEY: CDS
LOCATION: (136)..(1314)
US-09-305-914-1

Query Match 100.0%; Score 18; DB 4; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTCTGGC 18
DB 127 CCCGGAAGCAGCTCTGGC 110

RESULT 17
US-09-685-027-1/c
Sequence 1, Application US/09685027
Patent No. 6420118
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
APPLICANT: Hartwig, Wolfgang
TITLE OF INVENTION: Peptides and Peptidomimetics with
Structural Similarity to Human p53 That Activate p53
Function
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/685,027
FILING DATE: 10-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,542
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486,48439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-685-027-1
Query Match      100.0%; Score 18; DB 4; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 CCGGAGGCGAGTCTGGC 18
          |||
Db      127 CCGGAGGCGAGTCTGGC 110
```

```

RESULT 18
PCT-US95-15353-1/c
Sequence 1, Application PC/TUS9515353
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy
APPLICANT: and Biology
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
TITLE OF INVENTION: Tetramerization Domains
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15353
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/431,357
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/456,623
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
```

```

REFERENCE/DOCKET NUMBER: WST586CCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
PCT-US95-15353-1
```

```

Query Match      100.0%; Score 18; DB 5; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 CCGGAGGCGAGTCTGGC 18
          |||
Db      127 CCGGAGGCGAGTCTGGC 110
```

```

RESULT 19
US-09-404-879A-332
Sequence 332, Application US/09404879A
Patent No. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 332
LENGTH: 184
TYPE: DNA
ORGANISM: Homo sapiens
US-09-404-879A-332
```

```

Query Match      85.6%; Score 15.4; DB 4; Length 184;
Best Local Similarity 94.1%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 CCGGAGGCGAGTCTGGC 18
          |||
Db      112 CCGGAGGCGAGTCTGGC 128
```

```

RESULT 20
US-09-702-705-1634/c
Sequence 1634, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
```

/ CURRENT FILING DATE: 2000-10-30
/ NUMBER OF SEQ ID NOS: 1833
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1634
/ LENGTH: 447
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-702-705-1634

Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 73 CCGAAGGCACTCTGGC 57

RESULT 21
US-09-736-457-1634/c
/ Sequence 1634, Application US/09736457
/ Patent No. 6509448

GENERAL INFORMATION:

/ APPLICANT: Wang, Tonglong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darriek
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ APPLICANT: Fan, Liqun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.478C15
/ CURRENT APPLICATION NUMBER: US/09/736,457
/ CURRENT FILING DATE: 2000-12-13
/ NUMBER OF SEQ ID NOS: 1864
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1634
/ LENGTH: 447
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-736-457-1634

Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 73 CCGAAGGCACTCTGGC 57

RESULT 22
US-09-614-124B-1634/c
/ Sequence 1634, Application US/09614124B
/ Patent No. 6630578

GENERAL INFORMATION:

/ APPLICANT: Wang, Tonglong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darriek
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
/ FILE REFERENCE: 210121.478C9
/ CURRENT APPLICATION NUMBER: US/09/614,124B
/ CURRENT FILING DATE: 2001-07-11

/ NUMBER OF SEQ ID NOS: 1668
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1634
/ LENGTH: 447
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-614-124B-1634

Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 73 CCGAAGGCACTCTGGC 57

RESULT 23
US-09-671-325-1634/c
/ Sequence 1634, Application US/09671325
/ Patent No. 6667154

GENERAL INFORMATION:

/ APPLICANT: Wang, Tonglong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darriek
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ APPLICANT: Fan, Liqun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.478C12
/ CURRENT APPLICATION NUMBER: US/09/671,325
/ CURRENT FILING DATE: 2000-09-26
/ NUMBER OF SEQ ID NOS: 1825
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1634
/ LENGTH: 447
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-671-325-1634

Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 73 CCGAAGGCACTCTGGC 57

RESULT 24
US-09-385-982-206/c
/ Sequence 206, Application US/09385982
/ Patent No. 6262334

GENERAL INFORMATION:

/ APPLICANT: ENDBERG, WILSON O., ET AL.
/ TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
/ FILE REFERENCE: CCDNA-260XX
/ CURRENT APPLICATION NUMBER: US/09/385,982
/ CURRENT FILING DATE: 1999-08-30
/ EARLIER APPLICATION NUMBER: 09/328,111
/ EARLIER FILING DATE: 1999-06-08
/ EARLIER APPLICATION NUMBER: 60/117,393
/ EARLIER FILING DATE: 1999-01-27
/ EARLIER APPLICATION NUMBER: 60/098,639
/ EARLIER FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 544
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 206

LENGTH: 633
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(633)
OTHER INFORMATION: n = A,T,C or G
US-09-385-982-206

Query Match 85.6%; Score 15.4; DB 3; Length 633;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 426 CCGAAGGCACTCTGGC 410

RESULT 25
US-09-222-575-81
Sequence 81, Application US/09222575
Patent No. 6387697
GENERAL INFORMATION:
APPLICANT: Yugu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
FILE REFERENCE: 210121.470
CURRENT APPLICATION NUMBER: US/09/222.575
CURRENT FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Human
US-09-222-575-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 575 CCGAAGGCACTCTGGC 591

RESULT 26
US-09-389-681-81
Sequence 81, Application US/09389681A
Patent No. 6518237
GENERAL INFORMATION:
APPLICANT: Yugu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C3
CURRENT APPLICATION NUMBER: US/09/389.681A
CURRENT FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Homo sapien
US-09-389-681-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 575 CCGAAGGCACTCTGGC 591

RESULT 27
US-09-620-405B-81
Sequence 81, Application US/09620405B
Patent No. 6528054
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C8
CURRENT APPLICATION NUMBER: US/09/620.405B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Homo sapien
US-09-620-405B-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 575 CCGAAGGCACTCTGGC 591

RESULT 28
US-09-339-338-81
Sequence 81, Application US/09339338A
Patent No. 6573368
GENERAL INFORMATION:
APPLICANT: Yugu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C2
CURRENT APPLICATION NUMBER: US/09/339.338A
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Homo sapien
US-09-339-338-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 575 CCGAAGGCACTCTGGC 591

RESULT 29
US-09-433-826B-81

Sequence 81, Application US/09433826B
Patent No. 6579973
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C4
CURRENT APPLICATION NUMBER: US/09/433,826B
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 474
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Homo sapien
US-09-433-826B-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
DB 575 CCGAAGGCGAGTCTGGC 591

RESULT 30
US-09-604-287A-81
Sequence 81, Application US/09604287A
Patent No. 6586572
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C7
CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Homo sapien
US-09-604-287A-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
DB 575 CCGAAGGCGAGTCTGGC 591

RESULT 31
US-09-285-480-81
Sequence 81, Application US/09285480
Patent No. 6590076
GENERAL INFORMATION:
APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C1
CURRENT APPLICATION NUMBER: US/09/285,480
CURRENT FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 181
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Homo sapien
US-09-285-480-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
DB 575 CCGAAGGCGAGTCTGGC 591

RESULT 32
US-09-834-759-81
Sequence 81, Application US/09834759
Patent No. 6680197
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C9
CURRENT APPLICATION NUMBER: US/09/834,759
CURRENT FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Homo sapien
US-09-834-759-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
DB 575 CCGAAGGCGAGTCTGGC 591

RESULT 33
US-08-447-179-7/C
Sequence 7, Application US/08447179
Patent No. 5744303
GENERAL INFORMATION:
APPLICANT: 1990, Richard
APPLICANT: Friend, Stephen H.
APPLICANT: Prebourg, Thierry
APPLICANT: Ishioke, Chikashi
TITLE OF INVENTION: FUNCTIONAL ASSAY FOR TUMOR
TITLE OF INVENTION: SUPPRESSOR GENES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,179
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/046,033
FILING DATE: 12 APRIL 1993
APPLICATION NUMBER: 07/956,696
FILING DATE: 10 OCTOBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/159002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-447-179-7

Query Match 83.3%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAAGCAGCTGGC 18
DB 25 GGAAGCAGCTGGC 11

RESULT 34
US-09-445-247-21/c
Sequence 21, Application US/09445247
Patent No. 6410238
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy & Biology
Sakamuro, Daitoku
TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
(Bmi1) Compositions and Uses Therefor
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/445,247
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/870,126
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: M5T6D0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..108
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-445-247-21

Query Match 82.2%; Score 14.8; DB 4; Length 108;
Best Local Similarity 88.3%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
DB 36 CCCGGAAGCAGCTGGC 19

RESULT 35
US-08-094-071-1/c
Sequence 1, Application US/08094071
Patent No. 6083709
GENERAL INFORMATION:
APPLICANT: Reynolds, Frederick H.
APPLICANT: Sorvillo, John M.
APPLICANT: Zehab, Ron J.
APPLICANT: Stephenson, John R.
TITLE OF INVENTION: Immunoassay for Detection of
TITLE OF INVENTION: mutant p53 polypeptide in
TITLE OF INVENTION: biological fluids
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/094,071
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 719,172
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 649,566
FILING DATE: 01-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,776
FILING DATE: 17-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,837
FILING DATE: 18-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 885,627
FILING DATE: 23-JUL-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 767,862
FILING DATE: 21-AUG-1985

PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU 61540/86
FILING DATE: 18-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CA 516,260
FILING DATE: 19-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 86,111 527.7
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 195121/86
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NZ 217,209
FILING DATE: 14-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 23384-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 coop u:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
IMMEDIATE SOURCE:
CLONE: activated p53 oncogene
PUBLICATION INFORMATION:
AUTHORS: Harlow, E.
AUTHORS: Williamson, N. M.
AUTHORS: Ralston, R.
AUTHORS: Helfman, D. M.
AUTHORS: Adams, T. E.
TITLE: Molecular Cloning and In-Vitro
TITLE: Expression of a C-DNA Clone for Human
TITLE: Cellular Tumor Antigen P53
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 7
PAGES: 1601-1610
DATE: July-1985
US-08-094-071-1

Query Match 82.2%; Score 14.8; DB 3; Length 1757;
Best Local Similarity 88.9%; Pred.No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCGAAAGCAGCTGGC 18
DB 206 CCGGAAAGCAGCTGGC 189

RESULT 36
PCT-US92-00878-1/C
Sequence 1, Application PC/TUS9200878
GENERAL INFORMATION:
APPLICANT: Reynolds, Frederick H.
APPLICANT: Scivillio, John M.
APPLICANT: Zehnb, Ron J.
APPLICANT: Stephenson, John R.
TITLE OF INVENTION: Immunoassay for Detection of mutant p53
TITLE OF INVENTION: polypeptide in biological fluids
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham
STREET: 30 Rockefeller Plaza

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00878
FILING DATE: 19920131
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 719,172
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 649,566
FILING DATE: 01-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,776
FILING DATE: 17-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,837
FILING DATE: 18-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 885,627
FILING DATE: 23-JUL-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 767,862
FILING DATE: 21-AUG-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU 61540/86
FILING DATE: 18-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CA 516,260
FILING DATE: 19-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 86,111 527.7
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 195121/86
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NZ 217,209
FILING DATE: 14-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 23384-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 coop u:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
IMMEDIATE SOURCE:
CLONE: activated p53 oncogene
PUBLICATION INFORMATION:
AUTHORS: Harlow, E.
AUTHORS: Williamson, N. M.
AUTHORS: Ralston, R.
AUTHORS: Helfman, D. M.
AUTHORS: Adams, T. E.
TITLE: Molecular Cloning and In-Vitro Expression of a C-DNA
TITLE: Clone for Human Cellular Tumor Antigen P53

JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 7
PAGES: 1601-1610
DATE: July-1985
PCT-US92-00878-1

Query Match 82.2% Score 14.8; DB 5; Length 1757;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGGAGGAGGAGCTGGC 18
Db 206 CCGGAGGAGGAGCTGGC 189

RESULT 37
US-08-870-126-12/c
Sequence 12, Application US/08870126
Patent No. 6048702
GENERAL INFORMATION:
APPLICANT: Pendergast, George C.
APPLICANT: Sakamuro, Daitoku
TITLE OF INVENTION: Murine and Human Box-Dependent
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,126
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,972
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST60CUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8078 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: exon
LOCATION: 1841..1948
OTHER INFORMATION: /note= "putative.alt.exon"
FEATURE:
NAME/KEY: exon
LOCATION: 2409..2432
OTHER INFORMATION: /note= "putative.alt.exon"
FEATURE:
NAME/KEY: exon
LOCATION: 3308..3601

OTHER INFORMATION: /note= "putative.alt.exon"
FEATURE:
NAME/KEY: exon
LOCATION: 4613..4702
OTHER INFORMATION: /note= "exon 13"
FEATURE:
NAME/KEY: exon
LOCATION: 4944..5054
OTHER INFORMATION: /note= "exon 14"
FEATURE:
NAME/KEY: exon
LOCATION: 5334..5435
OTHER INFORMATION: /note= "exon 15"
FEATURE:
NAME/KEY: exon
LOCATION: 7223..7783
OTHER INFORMATION: /note= "exon 16"
US-08-870-126-12
Query Match 82.2% Score 14.8; DB 3; Length 8078;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGGAGGAGGAGCTGGC 18
Db 3529 CCGGAGGAGGAGCTGGC 3512

RESULT 38
US-09-445-247-12/c
Sequence 12, Application US/09445247
Patent No. 6410238
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy & Biology
Pendergast, George C.
Sakamuro, Daitoku
TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
(Bin1) Compositions and Uses Therefor
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/445,247
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/870,126
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST60DPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8078 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: exon
LOCATION: 1841..1948
OTHER INFORMATION: /note= "exon 12B"
FEATURE:
NAME/KEY: exon
LOCATION: 2409..2432
OTHER INFORMATION: /note= "exon 12C"
FEATURE:
NAME/KEY: exon
LOCATION: 3494..3601
OTHER INFORMATION: /note= "exon 12D"
FEATURE:
NAME/KEY: exon
LOCATION: 4613..4702
OTHER INFORMATION: /note= "exon 13"
FEATURE:
NAME/KEY: exon
LOCATION: 4944..5054
OTHER INFORMATION: /note= "exon 14"
FEATURE:
NAME/KEY: exon
LOCATION: 5334..5435
OTHER INFORMATION: /note= "exon 15"
NAME/KEY: exon
LOCATION: 7223..7783
OTHER INFORMATION: /note= "exon 16"
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-445-247-12

Query Match 82.2%; Score 14.8; DB 4; Length 8078;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGGAGGACGCTGCGC 18
Db 3529 CCGGAGGACGCTGCGC 3512

RESULT 39
US-08-652-972A-6/c
Sequence 6, Application US/08652972A
Patent No. 5723581
GENERAL INFORMATION:
APPLICANT: Prendergast, George C.
APPLICANT: Sakamuro, Daitoku
TITLE OF INVENTION: Murine and Human Box-Dependent
TITLE OF INVENTION: MYC-Interacting Protein (BIN1) and Uses Therefor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,972A
FILING DATE: 24-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST608USA
TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 14985 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: unsure
LOCATION: 1332
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE:
NAME/KEY: unsure
LOCATION: 3225
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE:
NAME/KEY: unsure
LOCATION: 7209
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE:
NAME/KEY: unsure
LOCATION: 11097
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE:
NAME/KEY: exon
LOCATION: 1..324
OTHER INFORMATION: /note= "Exon 1"
FEATURE:
NAME/KEY: exon
LOCATION: 325..1618
OTHER INFORMATION: /note= "Exon 2"
FEATURE:
NAME/KEY: exon
LOCATION: 1619..3174
OTHER INFORMATION: /note= "Exon 3"
FEATURE:
NAME/KEY: exon
LOCATION: 3175..4365
OTHER INFORMATION: /note= "Exon 4"
FEATURE:
NAME/KEY: exon
LOCATION: 4441..11518
OTHER INFORMATION: /note= "Exon 5"
FEATURE:
NAME/KEY: exon
LOCATION: 11519..11850
OTHER INFORMATION: /note= "Exon 6"
FEATURE:
NAME/KEY: exon
LOCATION: 11851..12240
OTHER INFORMATION: /note= "Exon 7"
FEATURE:
NAME/KEY: exon
LOCATION: 12241..14129
OTHER INFORMATION: /note= "Exon 8"
FEATURE:
NAME/KEY: exon
LOCATION: 14130..14985
OTHER INFORMATION: /note= "Exon 9"
US-08-652-972A-6

Query Match 82.2%; Score 14.8; DB 1; Length 14985;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGGAGGACGCTGCGC 18
Db 10738 CCGGAGGACGCTGCGC 10721

RESULT 40

PCT-US96-06231A-6/c
Sequence 6, Application PC/TUS9606231A
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy & Biology
TITLE OF INVENTION: Murine and Human Box-Dependent
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06231A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST60APCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 14985 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: unsure
LOCATION: 1332
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE:
NAME/KEY: unsure
LOCATION: 3225
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE:
NAME/KEY: unsure
LOCATION: 7209
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE:
NAME/KEY: unsure
LOCATION: 11097
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE:
NAME/KEY: exon
LOCATION: 325..1618
OTHER INFORMATION: /note= "Exon 2"
FEATURE:
NAME/KEY: exon
LOCATION: 1619..3174
OTHER INFORMATION: /note= "Exon 3"
FEATURE:
NAME/KEY: exon
LOCATION: 3175..4365
OTHER INFORMATION: /note= "Exon 4"
FEATURE:

NAME/KEY: exon
LOCATION: 4441..11518
OTHER INFORMATION: /note= "Exon 5"
FEATURE:
NAME/KEY: exon
LOCATION: 11519..11850
OTHER INFORMATION: /note= "Exon 6"
FEATURE:
NAME/KEY: exon
LOCATION: 11851..12240
OTHER INFORMATION: /note= "Exon 7"
FEATURE:
NAME/KEY: exon
LOCATION: 12241..14129
OTHER INFORMATION: /note= "Exon 8"
FEATURE:
NAME/KEY: exon
LOCATION: 14130..14985
OTHER INFORMATION: /note= "Exon 9"
PCT-US96-06231A-6
Query Match
Best Local Similarity 82.2%; Score 14.8; DB 5; Length 14985;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCGGAAAGCAGCTGCGC 18
DB 10738 CCGGAAAGCAGCTGCC 10721
RESULT 41
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2
Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 4403765;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCGGAAAGCAGCTGCGC 18
DB 1092940 CCGGAAAGCAGCTGCC 1092923
RESULT 42
US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 4411529;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGGAGGAGGAGTCTGAC 18
Db 1092941 CCGGAGGAGGAGTCTGAC 1092924

RESULT 43
US-09-621-976-11048/c
Sequence 11048, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Joubert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 11048
LENGTH: 252
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 148
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-11048

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 4; Length 252;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGAGGAGGAGTCTG 16
Db 107 CCGGAGGAGGAGTCTG 92

RESULT 44
US-08-256-077-3
Sequence 3, Application US/08256077
Patent No. 5654188
GENERAL INFORMATION:
APPLICANT: Elimeier, Wilfried
APPLICANT: Weith, Andreas
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,077
FILING DATE: 23-JUNE-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bismond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1360000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2640
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-256-077-3

Query Match
Best Local Similarity 80.0%; Score 14.4; DB 1; Length 360;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGAGGAGGAGTCTGAC 18
Db 53 CCGAGGAGGAGTCTGAC 68

RESULT 45
US-08-466-127-3
Sequence 3, Application US/08466127
Patent No. 5683878
GENERAL INFORMATION:
APPLICANT: Elimeier, Wilfried
APPLICANT: Weith, Andreas
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,127
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bismond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1360002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2640
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 1..357
US-08-466-127-3

Query Match
Best Local Similarity 80.0%; Score 14.4; DB 1; Length 360;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CGAAGCGAGTCTGGC 18
|||||
Db 53 CGAAGCGAGTCTGGC 68

RESULT 46
US-08-256-077-1
Sequence 1, Application US/08256077
Patent No. 5654188
GENERAL INFORMATION:
APPLICANT: Elimeier, Wilfried
APPLICANT: Weith, Andreas
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,077
FILING DATE: 23-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1360000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 982 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-256-077-1

Query Match
Best Local Similarity 80.0%; Score 14.4; DB 1; Length 982;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CGAAGCGAGTCTGGC 18
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Db 176 CGAAGCGAGTCTGGC 191

RESULT 47
US-08-466-127-1
Sequence 1, Application US/08466127
Patent No. 5683878
GENERAL INFORMATION:
APPLICANT: Elimeier, Wilfried
APPLICANT: Weith, Andreas
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,127
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1360002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 982 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 37...481
US-08-466-127-1

Query Match
Best Local Similarity 80.0%; Score 14.4; DB 1; Length 982;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CGAAGCGAGTCTGGC 18
|||||
Db 176 CGAAGCGAGTCTGGC 191

RESULT 48
US-09-566-921-7/c
Sequence 7, Application US/09566921
Patent No. 6682888
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 8137
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6682888 411474.10
NAME/KEY: unsure
LOCATION: 3488-3788
OTHER INFORMATION: a, t, c, g, or other
US-09-566-921-7

Query Match
Best Local Similarity 77.8%; Score 14; DB 4; Length 8137;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAAGGCACTTG 17
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Db 6246 GGAAGGCACTTG 6233

RESULT 49

US-08-721-986-1/c

; Sequence 1, Application US/08721986

; Patent No. 6103513

; GENERAL INFORMATION:

; APPLICANT: NICHOLSON, DONALD W.

; APPLICANT: ALI, AMBERDEEN

; APPLICANT: VAILLANCOURT, JOHN P.

; APPLICANT: MONDAY, NEIL A.

; TITLE OF INVENTION: DNA ENCODING PRECURSOR OF

; TITLE OF INVENTION: INTERLEUKIN-1BETA CONVERTING ENZYME -RELATED CYSTEINE

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: JOSEPH A. COPPOLA

; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE

; CITY: RAHWAY

; STATE: NEW JERSEY

; COUNTRY: U.S.A.

; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/721,986

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/225,487

; FILING DATE: 08-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: COPPOLA, JOSEPH A.

; REGISTRATION NUMBER: 38,413

; REFERENCE/DOCKET NUMBER: 19038

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 908-594-6734

; TELEFAX: 908-594-4720

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 157 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-721-986-1

QY 1 CCCGGAAGGCACTTG 17
|||||
Db 103 CCCGGAAGGCACTCG 87

Query Match 76.7%; Score 13.8; DB 3; Length 157;

Best Local Similarity 88.2%; Pred. No. 4.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 50

US-08-225-487A-1/c

; Sequence 1, Application US/08225487A

; Patent No. 6110701

; GENERAL INFORMATION:

; APPLICANT: NICHOLSON, DONALD W.

; APPLICANT: ALI, AMBERDEEN

; APPLICANT: VAILLANCOURT, JOHN P.

; APPLICANT: MONDAY, NEIL A.

; TITLE OF INVENTION: DNA ENCODING PRECURSOR OF

; TITLE OF INVENTION: INTERLEUKIN-1BETA CONVERTING ENZYME -RELATED CYSTEINE

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: JOSEPH A. COPPOLA

; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE

; CITY: RAHWAY

; STATE: NEW JERSEY

; COUNTRY: U.S.A.

; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/225,487A

; FILING DATE: 08-APR-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: COPPOLA, JOSEPH A.

; REGISTRATION NUMBER: 38,413

; REFERENCE/DOCKET NUMBER: 19038

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 908-594-6734

; TELEFAX: 908-594-4720

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 157 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-225-487A-1

QY 1 CCCGGAAGGCACTTG 17
|||||
Db 103 CCCGGAAGGCACTCG 87

Query Match 76.7%; Score 13.8; DB 3; Length 157;

Best Local Similarity 88.2%; Pred. No. 4.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Search completed: March 5, 2004, 01:18:20

Job time : 98 secs

DEFINITION AGENCOURT 1015199 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6528131
5', mRNA sequence.
ACCESSION BU902747
VERSION BU902747.1 GI:24084660
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 817)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM14126 row: c column: 11
High quality sequence stop: 688.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6528131"
/tissue_type="Telomysarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_71"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
ORIGIN
Query Match 100.0%; Score 18; DB 13; Length 817;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGAGGAGGAGCTCTGGC 18
DB 88 CCCGAGGAGGAGCTCTGGC 71
RESULT 48
BO224113 818 bp mRNA linear EST 02-MAY-2002
BO224113/c AGENCOURT_7558930 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6045260
DEFINITION 5', mRNA sequence.
ACCESSION BO224113
VERSION BO224113.1 GI:20405513
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 818)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM13289 row: c column: 21

FEATURES High quality sequence stop: 644.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6045260"
/tissue_type="Embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_92"
/note="Organ: testis; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dt primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
ORIGIN
Query Match 100.0%; Score 18; DB 13; Length 818;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGAGGAGGAGCTCTGGC 18
DB 112 CCCGAGGAGGAGCTCTGGC 95
RESULT 49
BO228424 832 bp mRNA linear EST 02-MAY-2002
BO228424/c AGENCOURT_7657440 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059449
DEFINITION 5', mRNA sequence.
ACCESSION BO228424
VERSION BO228424.1 GI:20409824
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 832)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DT/Genstar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM13326 row: c column: 02
High quality sequence stop: 611.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6059449"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_68"
/note="Organ: lung; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 100.0%; Score 18; DB 13; Length 832;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGAGGAGGAGCTCTGGC 18

Db 174 CCCGGAAGCAGCTGGC 157

RESULT 50
AU139600/c

847 bp mRNA linear EST 02-AUG-2002

LOCUS AU139600 PLACE1 Homo sapiens CDNA clone PLACE1010955 5', mRNA

DEFINITION

sequence.

ACCESSION

AU139600.1 GI:11001121

VERSION

EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 847)

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,

Yamamoto,U., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

HRI human CDNA project

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix

Research Institute; CDNA library construction; Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

Location/Qualifiers

1..847

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="PLACE1010955"

/tissue_type="Placenta"

/clone_lib="PLACE1"

/note="Vector: pME18SFL3"

ORIGIN

Query Match

100.0%; Score 18; DB 9; Length 847;

Best Local Similarity

100.0%; Pred. No. 6.1e+02;

Matches 18; Conservative

0; Mismatches 0; Indels 0; Caps 0;

QY 1

CCCGGAAGCAGCTGGC 18

Db 669

CCCGGAAGCAGCTGGC 652

Search completed: March 5, 2004, 01:16:44

Job time : 2545 secs